

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Guevera, Jr., Juan G.
Hoogeveen, Ron C.
Moore, Paul J.

(ii) TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS

(iii) NUMBER OF SEQUENCES: 229

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: P.O. Box 4433
(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: McMillian, Nabeela R.
(B) REGISTRATION NUMBER: P-43,363
(C) REFERENCE/DOCKET NUMBER: ARAG:003

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4536 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu Glu Glu Met Leu Glu Asn Val Ser Leu Val Cys Pro Lys Asp Ala
1 5 10 15

Thr Arg Phe Lys His Leu Arg Lys Tyr Thr Tyr Asn Tyr Glu Ala Glu
20 25 30

Ser Ser Ser Gly Val Pro Gly Thr Ala Asp Ser Arg Ser Ala Thr Arg
35 40 45

Ile Asn Cys Lys Val Glu Leu Glu Val Pro Gln Leu Cys Ser Phe Ile
50 55 60

Leu Lys Thr Ser Gln Cys Thr Leu Lys Glu Val Tyr Gly Phe Asn Pro
65 70 75 80

Glu Gly Lys Ala Leu Leu Lys Lys Thr Lys Asn Ser Glu Glu Phe Ala
85 90 95

Ala Ala Met Ser Arg Tyr Glu Leu Lys Leu Ala Ile Pro Glu Gly Lys
100 105 110

Gln Val Phe Leu Tyr Pro Glu Lys Asp Glu Pro Thr Tyr Ile Leu Asn
115 120 125

Ile Lys Arg Gly Ile Ile Ser Ala Leu Leu Val Pro Pro Glu Thr Glu
130 135 140

Glu Ala Lys Gln Val Leu Phe Leu Asp Thr Val Tyr Gly Asn Cys Ser
145 150 155 160

Thr His Phe Thr Val Lys Thr Arg Lys Gly Asn Val Ala Thr Glu Ile
165 170 175

Ser Thr Glu Arg Asp Leu Gly Gln Cys Asp Arg Phe Lys Pro Ile Arg
180 185 190

Thr Gly Ile Ser Pro Leu Ala Leu Ile Lys Gly Met Thr Arg Pro Leu
195 200 205

Ser Thr Leu Ile Ser Ser Gln Ser Cys Gln Tyr Thr Leu Asp Ala
210 215 220

Lys Arg Lys His Val Ala Glu Ala Ile Cys Lys Glu Gln His Leu Phe
225 230 235 240

Leu Pro Phe Ser Tyr Asn Asn Lys Tyr Gly Met Val Ala Gln Val Thr
245 250 255

Gln Thr Leu Lys Leu Glu Asp Thr Pro Lys Ile Asn Ser Arg Phe Phe
260 265 270

Gly Glu Gly Thr Lys Lys Met Gly Leu Ala Phe Glu Ser Thr Lys Ser
275 280 285

Thr Ser Pro Pro Lys Gln Ala Glu Ala Val Leu Lys Thr Leu Gln Glu
290 295 300

Leu Lys Lys Leu Thr Ile Ser Glu Gln Asn Ile Gln Arg Ala Asn Leu
305 310 315 320

Phe Asn Lys Leu Val Thr Glu Leu Arg Gly Leu Ser Asp Glu Ala Val
325 330 335

Thr Ser Leu Leu Pro Gln Leu Ile Glu Val Ser Ser Pro Ile Thr Leu
340 345 350

Gln Ala Leu Val Gln Cys Gly Gln Pro Gln Cys Ser Thr His Ile Leu
355 360 365

Gln Trp Leu Lys Arg Val His Ala Asn Pro Leu Leu Ile Asp Val Val
370 375 380

Thr Tyr Leu Val Ala Leu Ile Pro Glu Pro Ser Ala Gln Gln Leu Arg
385 390 395 400

Glu Ile Phe Asn Met Ala Arg Asp Gln Arg Ser Arg Ala Thr Leu Tyr
405 410 415

Ala Leu Ser His Ala Val Asn Asn Tyr His Lys Thr Asn Pro Thr Gly
420 425 430

Thr Gln Glu Leu Leu Asp Ile Ala Asn Tyr Leu Met Glu Gln Ile Gln
435 440 445

Asp Asp Cys Thr Gly Asp Glu Asp Tyr Thr Tyr Leu Ile Leu Arg Val
450 455 460

Ile Gly Asn Met Gly Gln Thr Met Glu Gln Leu Thr Pro Glu Leu Lys
465 470 475 480

Ser Ser Ile Leu Lys Cys Val Gln Ser Thr Lys Pro Ser Leu Met Ile
485 490 495

Gln Lys Ala Ala Ile Gln Ala Leu Arg Lys Met Glu Pro Lys Asp Lys
500 505 510

Asp Gln Glu Val Leu Leu Gln Thr Phe Leu Asp Asp Ala Ser Pro Gly
515 520 525

Asp Lys Arg Leu Ala Ala Tyr Leu Met Leu Met Arg Ser Pro Ser Gln
530 535 540

Ala Asp Ile Asn Lys Ile Val Gln Ile Leu Pro Trp Glu Gln Asn Glu
545 550 555 560

Gln Val Lys Asn Phe Val Ala Ser His Ile Ala Asn Ile Leu Asn Ser
 565 570 575

Glu Glu Leu Asp Ile Gln Asp Leu Lys Lys Leu Val Lys Glu Ala Leu
 580 585 590

Lys Glu Ser Gln Leu Pro Thr Val Met Asp Phe Arg Lys Phe Ser Arg
 595 600 605

Asn Tyr Gln Leu Tyr Lys Ser Val Ser Leu Pro Ser Leu Asp Pro Ala
 610 615 620

Ser Ala Lys Ile Glu Gly Asn Leu Ile Phe Asp Pro Asn Asn Tyr Leu
 625 630 635 640

Pro Lys Glu Ser Met Leu Lys Thr Thr Leu Thr Ala Phe Gly Phe Ala
 645 650 655

Ser Ala Asp Leu Ile Glu Ile Gly Leu Glu Gly Lys Gly Phe Glu Pro
 660 665 670

Thr Leu Glu Ala Leu Phe Gly Lys Gln Gly Phe Phe Pro Asp Ser Val
 675 680 685

Asn Lys Ala Leu Tyr Trp Val Asn Gly Gln Val Pro Asp Gly Val Ser
 690 695 700

Lys Val Leu Val Asp His Phe Gly Tyr Thr Lys Asp Asp Lys His Glu
 705 710 715 720

Gln Asp Met Val Asn Gly Ile Met Leu Ser Val Glu Lys Leu Ile Lys
 725 730 735

Asp Leu Lys Ser Lys Glu Val Pro Glu Ala Arg Ala Tyr Leu Arg Ile
 740 745 750

Leu Gly Glu Glu Leu Gly Phe Ala Ser Leu His Asp Leu Gln Leu Leu
 755 760 765

Gly Lys Leu Leu Leu Met Gly Ala Arg Thr Leu Gln Gly Ile Pro Gln
 770 775 780

Met Ile Gly Glu Val Ile Arg Lys Gly Ser Lys Asn Asp Phe Phe Leu
 785 790 795 800

His Tyr Ile Phe Met Glu Asn Ala Phe Glu Leu Pro Thr Gly Ala Gly
 805 810 815

Leu Gln Leu Gln Ile Ser Ser Gly Val Ile Ala Pro Gly Ala Lys
 820 825 830

Ala Gly Val Lys Leu Glu Val Ala Asn Met Gln Ala Glu Leu Val Ala
 835 840 845

Lys Pro Ser Val Ser Val Glu Phe Val Thr Asn Met Gly Ile Ile Ile
 850 855 860
 Pro Asp Phe Ala Arg Ser Gly Val Gln Met Asn Thr Asn Phe Phe His
 865 870 875 880
 Glu Ser Gly Leu Glu Ala His Val Ala Leu Lys Ala Gly Lys Leu Lys
 885 890 895
 Phe Ile Ile Pro Ser Pro Lys Arg Pro Val Lys Leu Leu Ser Gly Gly
 900 905 910
 Asn Thr Leu His Leu Val Ser Thr Thr Lys Thr Glu Val Ile Pro Pro
 915 920 925
 Leu Ile Glu Asn Arg Gln Ser Trp Ser Val Cys Lys Gln Val Phe Pro
 930 935 940
 Gly Leu Asn Tyr Cys Thr Ser Gly Ala Tyr Ser Asn Ala Ser Ser Thr
 945 950 955 960
 Asp Ser Ala Ser Tyr Tyr Pro Leu Thr Gly Asp Thr Arg Leu Glu Leu
 965 970 975
 Glu Leu Arg Pro Thr Gly Glu Ile Glu Gln Tyr Ser Val Ser Ala Thr
 980 985 990
 Tyr Glu Leu Gln Arg Glu Asp Arg Ala Leu Val Asp Thr Leu Lys Phe
 995 1000 1005
 Val Thr Gln Ala Glu Gly Ala Lys Gln Thr Glu Ala Thr Met Thr Phe
 1010 1015 1020
 Lys Tyr Asn Arg Gln Ser Met Thr Leu Ser Ser Glu Val Gln Ile Pro
 1025 1030 1035 1040
 Asp Phe Asp Val Asp Leu Gly Thr Ile Leu Arg Val Asn Asp Glu Ser
 1045 1050 1055
 Thr Glu Gly Lys Thr Ser Tyr Arg Leu Thr Leu Asp Ile Gln Asn Lys
 1060 1065 1070
 Lys Ile Thr Glu Val Ala Leu Met Gly His Leu Ser Cys Asp Thr Lys
 1075 1080 1085
 Glu Glu Arg Lys Ile Lys Gly Val Ile Ser Ile Pro Arg Leu Gln Ala
 1090 1095 1100
 Glu Ala Arg Ser Glu Ile Leu Ala His Trp Ser Pro Ala Lys Leu Leu
 1105 1110 1115 1120
 Leu Gln Met Asp Ser Ser Ala Thr Ala Tyr Gly Ser Thr Val Ser Lys
 1125 1130 1135

Arg Val Ala Trp His Tyr Asp Glu Glu Lys Ile Glu Phe Glu Trp Asn
1140 1145 1150

Thr Gly Thr Asn Val Asp Thr Lys Lys Met Thr Ser Asn Phe Pro Val
1155 1160 1165

Asp Leu Ser Asp Tyr Pro Lys Ser Leu His Met Tyr Ala Asn Arg Leu
1170 1175 1180

Leu Asp His Arg Val Pro Glu Thr Asp Met Thr Phe Arg His Val Gly
1185 1190 1195 1200

Ser Lys Leu Ile Val Ala Met Ser Ser Trp Leu Gln Lys Ala Ser Gly
1205 1210 1215

Ser Leu Pro Tyr Thr Gln Thr Leu Gln Asp His Leu Asn Ser Leu Lys
1220 1225 1230

Glu Phe Asn Leu Gln Asn Met Gly Leu Pro Asp Phe His Ile Pro Glu
1235 1240 1245

Asn Leu Phe Leu Lys Ser Asp Gly Arg Val Lys Tyr Thr Leu Asn Lys
1250 1255 1260

Asn Ser Leu Lys Ile Glu Ile Pro Leu Pro Phe Gly Gly Lys Ser Ser
1265 1270 1275 1280

Arg Asp Leu Lys Met Leu Glu Thr Val Arg Thr Pro Ala Leu His Phe
1285 1290 1295

Lys Ser Val Gly Phe His Leu Pro Ser Arg Glu Phe Gln Val Pro Thr
1300 1305 1310

Phe Thr Ile Pro Lys Leu Tyr Gln Leu Gln Val Pro Leu Leu Gly Val
1315 1320 1325

Leu Asp Leu Ser Thr Asn Val Tyr Ser Asn Leu Tyr Asn Trp Ser Ala
1330 1335 1340

Ser Tyr Ser Gly Gly Asn Thr Ser Thr Asp His Phe Ser Leu Arg Ala
1345 1350 1355 1360

Arg Tyr His Met Lys Ala Asp Ser Val Val Asp Leu Leu Ser Tyr Asn
1365 1370 1375

Val Gln Gly Ser Gly Glu Thr Thr Tyr Asp His Lys Asn Thr Phe Thr
1380 1385 1390

Leu Ser Cys Asp Gly Ser Leu Arg His Lys Phe Leu Asp Ser Asn Ile
1395 1400 1405

Lys Phe Ser His Val Glu Lys Leu Gly Asn Asn Pro Val Ser Lys Gly
1410 1415 1420

Leu Leu Ile Phe Asp Ala Ser Ser Ser Trp Gly Pro Gln Met Ser Ala
1425 1430 1435 1440

Ser Val His Leu Asp Ser Lys Lys Lys Gln His Leu Phe Val Lys Glu
1445 1450 1455

Val Lys Ile Asp Gly Gln Phe Arg Val Ser Ser Phe Tyr Ala Lys Gly
1460 1465 1470

Thr Tyr Gly Leu Ser Cys Gln Arg Asp Pro Asn Thr Gly Arg Leu Asn
1475 1480 1485

Gly Glu Ser Asn Leu Arg Phe Asn Ser Ser Tyr Leu Gln Gly Thr Asn
1490 1495 1500

Gln Ile Thr Gly Arg Tyr Glu Asp Gly Thr Leu Ser Leu Thr Ser Thr
1505 1510 1515 1520

Ser Asp Leu Gln Ser Gly Ile Ile Lys Asn Thr Ala Ser Leu Lys Tyr
1525 1530 1535

Glu Asn Tyr Glu Leu Thr Leu Lys Ser Asp Thr Asn Gly Lys Tyr Lys
1540 1545 1550

Asn Phe Ala Thr Ser Asn Lys Met Asp Met Thr Phe Ser Lys Gln Asn
1555 1560 1565

Ala Leu Leu Arg Ser Glu Tyr Gln Ala Asp Tyr Glu Ser Leu Arg Phe
1570 1575 1580

Phe Ser Leu Leu Ser Gly Ser Leu Asn Ser His Gly Leu Glu Leu Asn
1585 1590 1595 1600

Ala Asp Ile Leu Gly Thr Asp Lys Ile Asn Ser Gly Ala His Lys Ala
1605 1610 1615

Thr Leu Arg Ile Gly Gln Asp Gly Ile Ser Thr Ser Ala Thr Thr Asn
1620 1625 1630

Leu Lys Cys Ser Leu Leu Val Leu Glu Asn Glu Leu Asn Ala Glu Leu
1635 1640 1645

Gly Leu Ser Gly Ala Ser Met Lys Leu Thr Thr Asn Gly Arg Phe Arg
1650 1655 1660

Glu His Asn Ala Lys Phe Ser Leu Asp Gly Lys Ala Ala Leu Thr Glu
1665 1670 1675 1680

Leu Ser Leu Gly Ser Ala Tyr Gln Ala Met Ile Leu Gly Val Asp Ser
1685 1690 1695

Lys Asn Ile Phe Asn Phe Lys Val Ser Gln Glu Gly Leu Lys Leu Ser
1700 1705 1710

Asn Asp Met Met Gly Ser Tyr Ala Glu Met Lys Phe Asp His Thr Asn
1715 1720 1725

Ser Leu Asn Ile Ala Gly Leu Ser Leu Asp Phe Ser Ser Lys Leu Asp
1730 1735 1740

Asn Ile Tyr Ser Ser Asp Lys Phe Tyr Lys Gln Thr Val Asn Leu Gln
1745 1750 1755 1760

Leu Gln Pro Tyr Ser Leu Val Thr Thr Leu Asn Ser Asp Leu Lys Tyr
1765 1770 1775

Asn Ala Leu Asp Leu Thr Asn Asn Gly Lys Leu Arg Leu Glu Pro Leu
1780 1785 1790

Lys Leu His Val Ala Gly Asn Leu Lys Gly Ala Tyr Gln Asn Asn Glu
1795 1800 1805

Ile Lys His Ile Tyr Ala Ile Ser Ser Ala Ala Leu Ser Ala Ser Tyr
1810 1815 1820

Lys Ala Asp Thr Val Ala Lys Val Gln Gly Val Glu Phe Ser His Arg
1825 1830 1835 1840

Leu Asn Thr Asp Ile Ala Gly Leu Ala Ser Ala Ile Asp Met Ser Thr
1845 1850 1855

Asn Tyr Asn Ser Asp Ser Leu His Phe Ser Asn Val Phe Arg Ser Val
1860 1865 1870

Met Ala Pro Phe Thr Met Thr Ile Asp Ala His Thr Asn Gly Asn Gly
1875 1880 1885

Lys Leu Ala Leu Trp Gly Glu His Thr Gly Gln Leu Tyr Ser Lys Phe
1890 1895 1900

Leu Leu Lys Ala Glu Pro Leu Ala Phe Thr Phe Ser His Asp Tyr Lys
1905 1910 1915 1920

Gly Ser Thr Ser His His Leu Val Ser Arg Lys Ser Ile Ser Ala Ala
1925 1930 1935

Leu Glu His Lys Val Ser Ala Leu Leu Thr Pro Ala Glu Gln Thr Gly
1940 1945 1950

Thr Trp Lys Leu Lys Thr Gln Phe Asn Asn Asn Glu Tyr Ser Gln Asp
1955 1960 1965

Leu Asp Ala Tyr Asn Thr Lys Asp Lys Ile Gly Val Glu Leu Thr Gly
1970 1975 1980

Arg Thr Leu Ala Asp Leu Thr Leu Leu Asp Ser Pro Ile Lys Val Pro
1985 1990 1995 2000

Leu Leu Leu Ser Glu Pro Ile Asn Ile Ile Asp Ala Leu Glu Met Arg
2005 2010 2015

Asp Ala Val Glu Lys Pro Gln Glu Phe Thr Ile Val Ala Phe Val Lys
2020 2025 2030

Tyr Asp Lys Asn Gln Asp Val His Ser Ile Asn Leu Pro Phe Phe Glu
2035 2040 2045

Thr Leu Gln Glu Tyr Phe Glu Arg Asn Arg Gln Thr Ile Ile Val Val
2050 2055 2060

Val Glu Asn Val Gln Arg Asn Leu Lys His Ile Asn Ile Asp Gln Phe
2065 2070 2075 2080

Val Arg Lys Tyr Arg Ala Ala Leu Gly Lys Leu Pro Gln Gln Ala Asn
2085 2090 2095

Asp Tyr Leu Asn Ser Phe Asn Trp Glu Arg Gln Val Ser His Ala Lys
2100 2105 2110

Glu Lys Leu Thr Ala Leu Thr Lys Lys Tyr Arg Ile Thr Glu Asn Asp
2115 2120 2125

Ile Gln Ile Ala Leu Asp Asp Ala Lys Ile Asn Phe Asn Glu Lys Leu
2130 2135 2140

Ser Gln Leu Gln Thr Tyr Met Ile Gln Phe Asp Gln Tyr Ile Lys Asp
2145 2150 2155 2160

Ser Tyr Asp Leu His Asp Leu Lys Ile Ala Ile Ala Asn Ile Ile Asp
2165 2170 2175

Glu Ile Ile Glu Lys Leu Lys Ser Leu Asp Glu His Tyr His Ile Arg
2180 2185 2190

Val Asn Leu Val Lys Thr Ile His Asp Leu His Leu Phe Ile Glu Asn
2195 2200 2205

Ile Asp Phe Asn Lys Ser Gly Ser Ser Thr Ala Ser Trp Ile Gln Asn
2210 2215 2220

Val Asp Thr Lys Tyr Gln Ile Arg Ile Gln Ile Gln Glu Lys Leu Gln
2225 2230 2235 2240

Gln Leu Lys Arg His Ile Gln Asn Ile Asp Ile Gln His Leu Ala Gly
2245 2250 2255

Lys Leu Lys Gln His Ile Glu Ala Ile Asp Val Arg Val Leu Leu Asp
2260 2265 2270

Gln Leu Gly Thr Thr Ile Ser Phe Glu Arg Ile Asn Asp Val Leu Glu
2275 2280 2285

His Val Lys His Phe Val Ile Asn Leu Ile Gly Asp Phe Glu Val Ala
2290 2295 2300
Glu Lys Ile Asn Ala Phe Arg Ala Lys Val His Glu Leu Ile Glu Arg
2305 2310 2315 2320
Tyr Glu Val Asp Gln Gln Ile Gln Val Leu Met Asp Lys Leu Val Glu
2325 2330 2335
Leu Thr His Gln Tyr Lys Leu Lys Glu Thr Ile Gln Lys Leu Ser Asn
2340 2345 2350
Val Leu Gln Gln Val Lys Ile Lys Asp Tyr Phe Glu Lys Leu Val Gly
2355 2360 2365
Phe Ile Asp Asp Ala Val Lys Lys Leu Asn Glu Leu Ser Phe Lys Thr
2370 2375 2380
Phe Ile Glu Asp Val Asn Lys Phe Leu Asp Met Leu Ile Lys Lys Leu
2385 2390 2395 2400
Lys Ser Phe Asp Tyr His Gln Phe Val Asp Glu Thr Asn Asp Lys Ile
2405 2410 2415
Arg Glu Val Thr Gln Arg Leu Asn Gly Glu Ile Gln Ala Leu Glu Leu
2420 2425 2430
Pro Gln Lys Ala Glu Ala Leu Lys Leu Phe Leu Glu Glu Thr Lys Ala
2435 2440 2445
Thr Val Ala Val Tyr Leu Glu Ser Leu Gln Asp Thr Lys Ile Thr Leu
2450 2455 2460
Ile Ile Asn Trp Leu Gln Glu Ala Leu Ser Ser Ala Ser Leu Ala His
2465 2470 2475 2480
Met Lys Ala Lys Phe Arg Glu Thr Leu Glu Asp Thr Arg Asp Arg Met
2485 2490 2495
Tyr Asp Met Asp Ile Gln Gln Glu Leu Gln Arg Tyr Leu Ser Leu Val
2500 2505 2510
Gly Gln Val Tyr Ser Thr Leu Val Thr Tyr Ile Ser Asp Trp Trp Thr
2515 2520 2525
Leu Ala Ala Lys Asn Leu Thr Asp Phe Ala Glu Gln Tyr Ser Ile Gln
2530 2535 2540
Asp Trp Ala Lys Arg Met Lys Ala Leu Val Glu Gln Gly Phe Thr Val
2545 2550 2555 2560
Pro Glu Ile Lys Thr Ile Leu Gly Thr Met Pro Ala Phe Glu Val Ser
2565 2570 2575

Leu Gln Ala Leu Gln Lys Ala Thr Phe Gln Thr Pro Asp Phe Ile Val
2580 2585 2590

Pro Leu Thr Asp Leu Arg Ile Pro Ser Val Gln Ile Asn Phe Lys Asp
2595 2600 2605

Leu Lys Asn Ile Lys Ile Pro Ser Arg Phe Ser Thr Pro Glu Phe Thr
2610 2615 2620

Ile Leu Asn Thr Phe His Ile Pro Ser Phe Thr Ile Asp Phe Val Glu
2625 2630 2635 2640

Met Lys Val Lys Ile Ile Arg Thr Ile Asp Gln Met Gln Asn Ser Glu
2645 2650 2655

Leu Gln Trp Pro Val Pro Asp Ile Tyr Leu Arg Asp Leu Lys Val Glu
2660 2665 2670

Asp Ile Pro Leu Ala Arg Ile Thr Leu Pro Asp Phe Arg Leu Pro Glu
2675 2680 2685

Ile Ala Ile Pro Glu Phe Ile Ile Pro Thr Leu Asn Leu Asn Asp Phe
2690 2695 2700

Gln Val Pro Asp Leu His Ile Pro Glu Phe Gln Leu Pro His Ile Ser
2705 2710 2715 2720

His Thr Ile Glu Val Pro Thr Phe Gly Lys Leu Tyr Ser Ile Leu Lys
2725 2730 2735

Ile Gln Ser Pro Leu Phe Thr Leu Asp Ala Asn Ala Asp Ile Gly Asn
2740 2745 2750

Gly Thr Thr Ser Ala Asn Glu Ala Gly Ile Ala Ala Ser Ile Thr Ala
2755 2760 2765

Lys Gly Glu Ser Lys Leu Glu Val Leu Asn Phe Asp Phe Gln Ala Asn
2770 2775 2780

Ala Gln Leu Ser Asn Pro Lys Ile Asn Pro Leu Ala Leu Lys Glu Ser
2785 2790 2795 2800

Val Lys Phe Ser Ser Lys Tyr Leu Arg Thr Glu His Gly Ser Glu Met
2805 2810 2815

Leu Phe Phe Gly Asn Ala Ile Glu Gly Lys Ser Asn Thr Val Ala Ser
2820 2825 2830

Leu His Thr Glu Lys Asn Thr Leu Glu Leu Ser Asn Gly Val Ile Val
2835 2840 2845

Lys Ile Asn Asn Gln Leu Thr Leu Asp Ser Asn Thr Lys Tyr Phe His
2850 2855 2860

Lys Leu Asn Ile Pro Lys Leu Asp Phe Ser Ser Gln Ala Asp Leu Arg
2865 2870 2875 2880

Asn Glu Ile Lys Thr Leu Leu Lys Ala Gly His Ile Ala Trp Thr Ser
2885 2890 2895

Ser Gly Lys Gly Ser Trp Lys Trp Ala Cys Pro Arg Phe Ser Asp Glu
2900 2905 2910

Gly Thr His Glu Ser Gln Ile Ser Phe Thr Ile Glu Gly Pro Leu Thr
2915 2920 2925

Ser Phe Gly Leu Ser Asn Lys Ile Asn Ser Lys His Leu Arg Val Asn
2930 2935 2940

Gln Asn Leu Val Tyr Glu Ser Gly Ser Leu Asn Phe Ser Lys Leu Glu
2945 2950 2955 2960

Ile Gln Ser Gln Val Asp Ser Gln His Val Gly His Ser Val Leu Thr
2965 2970 2975

Ala Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala Glu Phe Thr Gly
2980 2985 2990

Arg His Asp Ala His Leu Asn Gly Lys Val Ile Gly Thr Leu Lys Asn
2995 3000 3005

Ser Leu Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr Ala Ser Thr Asn
3010 3015 3020

Asn Glu Gly Asn Leu Lys Val Arg Phe Pro Leu Arg Leu Thr Gly Lys
3025 3030 3035 3040

Ile Asp Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser Pro Ser Ala Gln
3045 3050 3055

Gln Ala Ser Trp Gln Val Ser Ala Arg Phe Asn Gln Tyr Lys Tyr Asn
3060 3065 3070

Gln Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His Val
3075 3080 3085

Gly Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile Pro Leu Thr
3090 3095 3100

Ile Pro Glu Met Arg Leu Pro Tyr Thr Ile Ile Thr Thr Pro Pro Leu
3105 3110 3115 3120

Lys Asp Phe Ser Leu Trp Glu Lys Thr Gly Leu Lys Glu Phe Leu Lys
3125 3130 3135

Thr Thr Lys Gln Ser Phe Asp Leu Ser Val Lys Ala Gln Tyr Lys Lys
3140 3145 3150

Asn Lys His Arg His Ser Ile Thr Asn Pro Leu Ala Val Leu Cys Glu
3155 3160 3165

Phe Ile Ser Gln Ser Ile Lys Ser Phe Asp Arg His Phe Glu Lys Asn
3170 3175 3180

Arg Asn Asn Ala Leu Asp Phe Val Thr Lys Ser Tyr Asn Glu Thr Lys
3185 3190 3195 3200

Ile Lys Phe Asp Lys Tyr Lys Ala Glu Lys Ser His Asp Glu Leu Pro
3205 3210 3215

Arg Thr Phe Gln Ile Pro Gly Tyr Thr Val Pro Val Val Asn Val Glu
3220 3225 3230

Val Ser Pro Phe Thr Ile Glu Met Ser Ala Phe Gly Tyr Val Phe Pro
3235 3240 3245

Lys Ala Val Ser Met Pro Ser Phe Ser Ile Leu Gly Ser Asp Val Arg
3250 3255 3260

Val Pro Ser Tyr Thr Leu Ile Leu Pro Ser Leu Glu Leu Pro Val Leu
3265 3270 3275 3280

His Val Pro Arg Asn Leu Lys Leu Ser Leu Pro His Phe Lys Glu Leu
3285 3290 3295

Cys Thr Ile Ser His Ile Phe Ile Pro Ala Met Gly Asn Ile Thr Tyr
3300 3305 3310

Asp Phe Ser Phe Lys Ser Ser Val Ile Thr Leu Asn Thr Asn Ala Glu
3315 3320 3325

Leu Phe Asn Gln Ser Asp Ile Val Ala His Leu Leu Ser Ser Ser Ser
3330 3335 3340

Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr Thr Arg Leu
3345 3350 3355 3360

Thr Arg Lys Arg Gly Leu Lys Leu Ala Thr Ala Leu Ser Leu Ser Asn
3365 3370 3375

Lys Phe Val Glu Gly Ser His Asn Ser Thr Val Ser Leu Thr Thr Lys
3380 3385 3390

Asn Met Glu Val Ser Val Ala Lys Thr Thr Lys Ala Glu Ile Pro Ile
3395 3400 3405

Leu Arg Met Asn Phe Lys Gln Glu Leu Asn Gly Asn Thr Lys Ser Lys
3410 3415 3420

Pro Thr Val Ser Ser Met Glu Phe Lys Tyr Asp Phe Asn Ser Ser
3425 3430 3435 3440

Met Leu Tyr Ser Thr Ala Lys Gly Ala Val Asp His Lys Leu Ser Leu
3445 3450 3455

Glu Ser Leu Thr Ser Tyr Phe Ser Ile Glu Ser Ser Thr Lys Gly Asp
3460 3465 3470

Val Lys Gly Ser Val Leu Ser Arg Glu Tyr Ser Gly Thr Ile Ala Ser
3475 3480 3485

Glu Ala Asn Thr Tyr Leu Asn Ser Lys Ser Thr Arg Ser Ser Val Lys
3490 3495 3500

Leu Gln Gly Thr Ser Lys Ile Asp Asp Ile Trp Asn Leu Glu Val Lys
3505 3510 3515 3520

Glu Asn Phe Ala Gly Glu Ala Thr Leu Gln Arg Ile Tyr Ser Leu Trp
3525 3530 3535

Glu His Ser Thr Lys Asn His Leu Gln Leu Glu Gly Leu Phe Phe Thr
3540 3545 3550

Asn Gly Glu His Thr Ser Lys Ala Thr Leu Glu Leu Ser Pro Trp Gln
3555 3560 3565

Met Ser Ala Leu Val Gln Val His Ala Ser Gln Pro Ser Ser Phe His
3570 3575 3580

Asp Phe Pro Asp Leu Gly Gln Glu Val Ala Leu Asn Ala Asn Thr Lys
3585 3590 3595 3600

Asn Gln Lys Ile Arg Trp Lys Asn Glu Val Arg Ile His Ser Gly Ser
3605 3610 3615

Phe Gln Ser Gln Val Glu Leu Ser Asn Asp Gln Glu Lys Ala His Leu
3620 3625 3630

Asp Ile Ala Gly Ser Leu Glu Gly His Leu Arg Phe Leu Lys Asn Ile
3635 3640 3645

Ile Leu Pro Val Tyr Asp Lys Ser Leu Trp Asp Phe Leu Lys Leu Asp
3650 3655 3660

Val Thr Thr Ser Ile Gly Arg Arg Gln His Leu Arg Val Ser Thr Ala
3665 3670 3675 3680

Phe Val Tyr Thr Lys Asn Pro Asn Gly Tyr Ser Phe Ser Ile Pro Val
3685 3690 3695

Lys Val Leu Ala Asp Lys Phe Ile Thr Pro Gly Leu Lys Leu Asn Asp
3700 3705 3710

Leu Asn Ser Val Leu Val Met Pro Thr Phe His Val Pro Phe Thr Asp
3715 3720 3725

Leu Gln Val Pro Ser Cys Lys Leu Asp Phe Arg Glu Ile Gln Ile Tyr
3730 3735 3740

Lys Lys Leu Arg Thr Ser Ser Phe Ala Leu Asn Leu Pro Thr Leu Pro
3745 3750 3755 3760

Glu Val Lys Phe Pro Glu Val Asp Val Leu Thr Lys Tyr Ser Gln Pro
3765 3770 3775

Glu Asp Ser Leu Ile Pro Phe Phe Glu Ile Thr Val Pro Glu Ser Gln
3780 3785 3790

Leu Thr Val Ser Gln Phe Thr Leu Pro Lys Ser Val Ser Asp Gly Ile
3795 3800 3805

Ala Ala Leu Asp Leu Asn Ala Val Ala Asn Lys Ile Ala Asp Phe Glu
3810 3815 3820

Leu Pro Thr Ile Ile Val Pro Glu Gln Thr Ile Glu Ile Pro Ser Ile
3825 3830 3835 3840

Lys Phe Ser Val Pro Ala Gly Ile Val Ile Pro Ser Phe Gln Ala Leu
3845 3850 3855

Thr Ala Arg Phe Glu Val Asp Ser Pro Val Tyr Asn Ala Thr Trp Ser
3860 3865 3870

Ala Ser Leu Lys Asn Lys Ala Asp Tyr Val Glu Thr Val Leu Asp Ser
3875 3880 3885

Thr Cys Ser Ser Thr Val Gln Phe Leu Glu Tyr Glu Leu Asn Val Leu
3890 3895 3900

Gly Thr His Lys Ile Glu Asp Gly Thr Leu Ala Ser Lys Thr Lys Gly
3905 3910 3915 3920

Thr Leu Ala His Arg Asp Phe Ser Ala Glu Tyr Glu Glu Asp Gly Lys
3925 3930 3935

Phe Glu Gly Leu Gln Glu Trp Glu Gly Lys Ala His Leu Asn Ile Lys
3940 3945 3950

Ser Pro Ala Phe Thr Asp Leu His Leu Arg Tyr Gln Lys Asp Lys Lys
3955 3960 3965

Gly Ile Ser Thr Ser Ala Ala Ser Pro Ala Val Gly Thr Val Gly Met
3970 3975 3980

Asp Met Asp Glu Asp Asp Asp Phe Ser Lys Trp Asn Phe Tyr Tyr Ser
3985 3990 3995 4000

Pro Gln Ser Ser Pro Asp Lys Lys Leu Thr Ile Phe Lys Thr Glu Leu
4005 4010 4015

Arg Val Arg Glu Ser Asp Glu Glu Thr Gln Ile Lys Val Asn Trp Glu
4020 4025 4030

Glu Glu Ala Ala Ser Gly Leu Leu Thr Ser Leu Lys Asp Asn Val Pro
4035 4040 4045

Lys Ala Thr Gly Val Leu Tyr Asp Tyr Val Asn Lys Tyr His Trp Glu
4050 4055 4060

His Thr Gly Leu Thr Leu Arg Glu Val Ser Ser Lys Leu Arg Arg Asn
4065 4070 4075 4080

Leu Gln Asn Asn Ala Glu Trp Val Tyr Gln Gly Ala Ile Arg Gln Ile
4085 4090 4095

Asp Asp Ile Asp Val Arg Phe Gln Lys Ala Ala Ser Gly Thr Thr Gly
4100 4105 4110

Thr Tyr Gln Glu Trp Lys Asp Lys Ala Gln Asn Leu Tyr Gln Glu Leu
4115 4120 4125

Leu Thr Gln Glu Gly Gln Ala Ser Phe Gln Gly Leu Lys Asp Asn Val
4130 4135 4140

Phe Asp Gly Leu Val Arg Val Thr Gln Lys Phe His Met Lys Val Lys
4145 4150 4155 4160

His Leu Ile Asp Ser Leu Ile Asp Phe Leu Asn Phe Pro Arg Phe Gln
4165 4170 4175

Phe Pro Gly Lys Pro Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met
4180 4185 4190

Phe Ile Arg Glu Val Gly Thr Val Leu Ser Gln Val Tyr Ser Lys Val
4195 4200 4205

His Asn Gly Ser Glu Ile Leu Phe Ser Tyr Phe Gln Asp Leu Val Ile
4210 4215 4220

Thr Leu Pro Phe Glu Leu Arg Lys His Lys Leu Ile Asp Val Ile Ser
4225 4230 4235 4240

Met Tyr Arg Glu Leu Leu Lys Asp Leu Ser Lys Glu Ala Gln Glu Val
4245 4250 4255

Phe Lys Ala Ile Gln Ser Leu Lys Thr Thr Glu Val Leu Arg Asn Leu
4260 4265 4270

Gln Asp Leu Leu Gln Phe Ile Phe Gln Leu Ile Glu Asp Asn Ile Lys
4275 4280 4285

Gln Leu Lys Glu Met Lys Phe Thr Tyr Leu Ile Asn Tyr Ile Gln Asp
4290 4295 4300

Glu Ile Asn Thr Ile Phe Asn Asp Tyr Ile Pro Tyr Val Phe Lys Leu
 4305 4310 4315 4320

 Leu Lys Glu Asn Leu Cys Leu Asn Leu His Lys Phe Asn Glu Phe Ile
 4325 4330 4335

 Gln Asn Glu Leu Gln Glu Ala Ser Gln Glu Leu Gln Gln Ile His Gln
 4340 4345 4350

 Tyr Ile Met Ala Leu Arg Glu Glu Tyr Phe Asp Pro Ser Ile Val Gly
 4355 4360 4365

 Trp Thr Val Lys Tyr Tyr Glu Leu Glu Glu Lys Ile Val Ser Leu Ile
 4370 4375 4380

 Lys Asn Leu Leu Val Ala Leu Lys Asp Phe His Ser Glu Tyr Ile Val
 4385 4390 4395 4400

 Ser Ala Ser Asn Phe Thr Ser Gln Leu Ser Ser Gln Val Glu Gln Phe
 4405 4410 4415

 Leu His Arg Asn Ile Gln Glu Tyr Leu Ser Ile Leu Thr Asp Pro Asp
 4420 4425 4430

 Gly Lys Gly Lys Glu Lys Ile Ala Glu Leu Ser Ala Thr Ala Gln Glu
 4435 4440 4445

 Ile Ile Lys Ser Gln Ala Ile Ala Thr Lys Lys Ile Ile Ser Asp Tyr
 4450 4455 4460

 His Gln Gln Phe Arg Tyr Lys Leu Gln Asp Phe Ser Asp Gln Leu Ser
 4465 4470 4475 4480

 Asp Tyr Tyr Glu Lys Phe Ile Ala Glu Ser Lys Arg Leu Ile Asp Leu
 4485 4490 4495

 Ser Ile Gln Asn Tyr His Thr Phe Leu Ile Tyr Ile Thr Glu Leu Leu
 4500 4505 4510

 Lys Lys Leu Gln Ser Thr Thr Val Met Asn Pro Tyr Met Lys Leu Ala
 4515 4520 4525

 Pro Gly Glu Leu Thr Ile Ile Leu
 4530 4535

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Xaa Pro
1

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys Tyr Thr Tyr Asn Tyr Glu Ala Glu Ser Ser Ser Gly Val Pro Gly
1 5 10 15

Thr Ala Asp Ser Arg Ser Ala Thr Arg Ile Asn Cys Lys Val Glu Leu
20 25 30

Glu Val Pro Gln Leu Cys Ser Phe Ile Leu Lys Thr Ser Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Tyr Asp Phe Asn Tyr Pro Ile Lys Lys Asp Ser Ser Ser Gln Leu
1 5 10 15

Leu Ser Val Gln Gln Gly Glu Thr Ile Tyr Ile Leu Asn Lys Asn Ser
20 25 30

Ser Gly Trp Trp Asp Gly Leu Val Ile Asp Asp Ser Asn
35 40 45

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Tyr Gly Phe Asn Pro Glu Gly Lys Ala Leu Leu Lys Lys Thr Lys
1 5 10 15

Asn Ser Glu Glu Phe Ala Ala Met Ser Arg Tyr Glu Leu Lys Leu
20 25 30

Ala Ile Pro Glu Gly Lys Gln Val Phe Leu Tyr Pro Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys
1 5 10 15

Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn His Tyr Asn Gly Glu Trp
20 25 30

Cys Glu Ala Gln Thr Lys Asn Gly Gln Gly Trp Val Pro Ser Asn
35 40 45

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Leu Pro Phe Ser Tyr Asn Asn Lys Tyr Gly Met Val Ala Gln Val
1 5 10 15

Thr Gln Thr Leu Lys Leu Glu Asp Thr Pro Lys Ile Asn Ser Arg Phe
20 25 30

Phe Gly Glu Gly Thr Lys Lys Met Gly Leu Ala Phe
35 40

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Phe Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu Thr Phe Thr Lys
1 5 10 15

Ser Ala Ile Ile Gln Asn Val Glu Lys Gln Glu Gly Gly Trp Trp Arg
20 25 30

Gly Asp Tyr Gly Gly Lys Lys Gln Leu Trp Phe
35 40

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Phe Leu Pro Phe Ser Tyr Asn Asn Lys Tyr Gly Met Val Ala Gln Val
1 5 10 15

Thr Gln Thr Leu Lys Leu Glu Asp Thr Pro Lys Ile Asn Ser Arg Phe
20 25 30

Phe Gly Glu Gly Thr Lys Lys Met Gly Leu Ala Phe Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu Gly Phe Glu Lys
1 5 10 15

Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu Trp Trp Lys Ala
20 25 30

Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro Phe Asn
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Tyr Thr Tyr Leu Ile Leu Arg Val Ile Gly Asn Met Gly Gln Thr Met
1 5 10 15

Glu Gln Leu Thr Pro Glu Leu Lys Ser Ser Ile Leu Lys Cys Val Gln
20 25 30

Ser Thr Lys Pro Ser Leu Met Ile Gln Lys Ala Ala Ile Gln Ala Leu
35 40 45

Arg Lys Met Glu Pro Lys Asp Lys Asp Gln Glu Val Leu Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val Val Ala Leu Phe Asp Tyr Ala Ala Val Asn Asp Arg Asp Leu Gln
1 5 10 15

Val Leu Lys Gly Glu Lys Leu Gln Val Leu Arg Ser Thr Gly Asp Trp
20 25 30

Trp Leu Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser
35 40 45

Asn Phe Val Ala Pro
50

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Phe Gly Phe Ala Ser Ala Asp Leu Ile Glu Ile Gly Leu Glu Gly
1 5 10 15

Lys Gly Phe Glu Pro Thr Leu Glu Ala Leu Phe Gly Lys Gln Gly Phe
20 25 30

Phe Pro Asp Ser Val Asn Lys Ala Leu Tyr Trp Val Asn Gly Gln Val
35 40 45

Pro Asp
50

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Tyr Asp Phe Ala Ala Glu Asn Pro Asp Glu Leu Thr Phe Asn Glu
1 5 10 15

Gly Ala Val Val Thr Val Ile Asn Lys Ser Asn Pro Asp Trp Trp Glu
20 25 30

Gly Glu Leu Asn Gly Gln Arg Gly Val Phe Pro Ala Ser Tyr Val Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Gly Tyr Thr Lys Asp Asp Lys His Glu Gln Asp Met Val Asn Gly
1 5 10 15
Ile Met Leu Ser Val Glu Lys Leu Ile Lys Asp Leu Lys Ser Lys Glu
20 25 30
Val Pro Glu Ala Arg Ala Tyr Leu Arg Ile Leu Gly Glu Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Asp Tyr Lys Lys Glu Glu Asp Ile Asp Leu His Leu Gly Asp
1 5 10 15
Ile Leu Thr Val Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp
20 25 30
Gly Gln Glu Ala Lys Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn
35 40 45
Glu

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Asp Tyr His Gln Phe Val Asp Glu Thr Asn Asp Lys Ile Arg Glu
1 5 10 15
Val Thr Gln Arg Leu Asn Gly Glu Ile Gln Ala Leu Glu Leu Pro Gln
20 25 30
Lys Ala Glu Ala Leu Lys Leu Phe Leu Glu Glu Thr Lys Ala Thr Val
35 40 45
Ala Val Tyr Leu
50

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys Lys Gly
1 5 10 15

Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp Trp Lys Val
20 25 30

Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala Tyr Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Asp Met Asp Ile Gln Gln Glu Leu Gln Arg Tyr Leu Ser Leu Val
1 5 10 15

Gly Gln Val Tyr Ser Thr Leu Val Thr Tyr Ile Ser Asp Trp Trp Thr
20 25 30

Leu Ala Ala Lys Asn Leu Thr Asp Phe Ala Glu Gln Tyr Ser Ile Gln
35 40 45

Asp Trp Ala
50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Phe Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu Thr Phe Thr Lys Ser
1 5 10 15

Ala Ile Ile Gln Asn Val Glu Lys Gln Asp Gly Gly Trp Trp Arg Gly
20 25 30

Asp Tyr Gly Gly Lys Lys Gln Leu Trp Phe Pro Ser Asn Tyr Val Glu
35 40 45

Glu Met Ile
50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Tyr Asp Met Asp Ile Gln Gln Glu Leu Gln Arg Tyr Leu Ser Leu Val
1 5 10 15

Gly Gln Val Tyr Ser Thr Leu Val Thr Tyr Ile Ser Asp Trp Trp Thr
20 25 30

Leu Ala Ala Lys Asn Leu Thr Asp Phe Ala Glu Gln Tyr Ser Ile Gln
35 40 45

Asp Trp Ala Lys Arg Met Lys
50 55

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Gln Asp Tyr Glu Pro Arg Leu Thr Asp Glu Ile Arg Ile Ser Leu
1 5 10 15

Gly Glu Lys Val Lys Ile Leu Ala Thr His Thr Asp Gly Trp Cys Leu
20 25 30

Val Glu Lys Cys Asn Thr Arg Lys Gly Thr Ile His Val Ser Val Asp
35 40 45

Asp Lys Arg Tyr Leu
50

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Thr Phe Thr Lys Gly
1 5 10 15

Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly Asp Trp Trp Glu Ala
20 25 30

Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile Pro Ser Asn Tyr Val
35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Thr Tyr Asp Phe Ser Phe Lys Ser Ser Val Ile Thr Leu Asn Thr Asn
1 5 10 15

Ala Glu Leu Phe Asn Gln Ser Asp Ile Val Ala His Leu Leu Ser Ser
20 25 30

Ser Ser Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp	Phe	Asn	Tyr	Pro	Ile	Lys	Lys	Asp	Ser	Ser	Ser	Gln	Leu	Leu	Ser
1															15
				5											
Val	Gln	Gln	Gly	Glu	Thr	Ile	Tyr	Ile	Leu	Asn	Lys	Asn	Ser	Ser	Gly
															30
					20										
Trp	Trp	Asp	Gly	Leu	Val	Ile	Asp	Asp	Ser	Asn	Gly	Lys	Val	Asn	
															45
					35										
						40									

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys	Tyr	Asp	Phe	Asn	Ser	Ser	Met	Leu	Tyr	Ser	Thr	Ala	Lys	Gly	Ala
1															15
							5								
Val	Asp	His	Lys	Leu	Ser	Leu	Glu	Ser	Leu	Thr	Ser	Tyr	Phe	Ser	Ile
															30
					20										
Glu	Ser	Ser	Thr	Lys	Gly	Asp	Val	Lys	Gly	Ser	Val	Leu	Ser	Arg	Glu
															45
					35										
						40									
							45								
								Tyr							

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu	Pro	Tyr	Val	Ala	Ile	Lys	Ala	Tyr	Thr	Ala	Val	Glu	Gly	Asp	Glu
1															15
Val	Ser	Leu	Leu	Glu	Gly	Glu	Ala	Val	Glu	Val	Ile	His	Lys	Leu	Leu
															30
					20										
						25									

Asp Gly Trp Trp Val Ile Arg Lys Asp Asp Val Thr Gly Tyr Phe Pro
35 40 45

Ser Met Tyr Leu
50

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Trp Asp Phe Leu Lys Leu Asp Val Thr Thr Ser Ile Gly Arg Arg
1 5 10 15

Gln His Leu Arg Val Ser Thr Ala Phe Val Tyr Thr Lys Asn Pro Asn
20 25 30

Gly Tyr Ser Phe Ser Ile Pro Val Lys Val Leu Ala Asp Lys Phe Ile
35 40 45

Thr Pro Gly Leu Lys Leu
50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Tyr Asp Phe Lys Ala Glu Lys Ala Asp Glu Leu Thr Thr Tyr Val
1 5 10 15

Gly Glu Asn Leu Phe Ile Cys Ala His His Asn Cys Glu Trp Phe Ile
20 25 30

Ala Lys Pro Ile Gly Arg Leu Gly Gly Pro Gly Leu Val Pro Val Gly
35 40 45

Phe Val Ser Ile Ile Asp Ile
50 55

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Val Leu Tyr Asp Tyr Val Asn Lys Tyr His Trp Glu His Thr Gly Leu
1 5 10 15

Thr Leu Arg Glu Val Ser Ser Lys Leu Arg Arg Asn Leu Gln Asn Asn
20 25 30

Ala Glu Trp Val Tyr Gln Gly Ala Ile Arg Gln Ile Asp Asp Ile
35 40 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Val Leu Tyr Asp Phe Lys Ala Glu Lys Ala Asp Glu Leu Thr Thr Tyr
1 5 10 15

Val Gly Glu Asn Leu Phe Ile Cys Ala His His Asn Cys Glu Trp Phe
20 25 30

Ile Ala Lys Pro Ile Gly Arg Leu
35 40

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Pro Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met Phe Ile Arg
1 5 10 15

Glu Val Gly Thr Val Leu Ser Gln Val Tyr Ser Lys Val His Asn Gly
20 25 30

Ser Glu Ile Leu Phe Ser Tyr Phe Gln Asp Leu
35 40

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Leu Phe Gly Phe Val Pro Glu Thr Lys Glu Glu Leu Gln Val Met Pro
1 5 10 15

Gly Asn Ile Val Phe Val Leu Lys Lys Gly Asn Asp Asn Trp Ala Thr
20 25 30

Val Met Phe Asn Gly Gln Lys Gly Leu Val Pro Cys Asn Tyr Leu Glu
35 40 45

Pro Val Glu Leu
50

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Lys Pro Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met Phe Ile
1 5 10 15

Arg Glu Val Gly Thr Val Leu Ser Gln Val Tyr Ser Lys Val His Asn
20 25 30

Gly Ser Glu Ile Leu Phe Ser Tyr Phe Gln Asp
35 40

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Lys Phe Asp Tyr Val Ala Gln Gln Glu Glu Leu Asp Ile Lys
1 5 10 15

Lys Asn Glu Arg Leu Trp Leu Leu Asp Asp Ser Lys Ser Trp Trp Arg
20 25 30

Val Arg Asn Ser Met Asn Lys Thr Gly Phe Val Pro Ser Asn Tyr Val
35 40 45

Glu Arg Lys Asn
50

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp Tyr His Ala Ser Leu Thr Arg Ala Gln Ala Glu His Met Leu Met
1 5 10 15

Arg Val Pro Arg Asp Gly Ala Phe Leu Val Arg Lys Arg Asn Glu Pro
20 25 30

Asn Ser Tyr Ala Ile Ser Phe Arg Ala Glu Gly Lys Ile Lys His Cys
35 40 45

Arg Val Gln Gln Glu Gly Thr Val Met Leu Gly Asn Ser Glu Phe Asp
50 55 60

Ser Leu Val Asp Leu Ile Ser Tyr Tyr Glu Lys His Pro Leu Tyr Arg
65 70 75 80

Lys Met Lys Leu Arg
85

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Phe Gly Glu Gly Thr Lys Lys Met Gly Leu Ala Phe Glu Ser Thr
1 5 10 15

Lys Ser Thr Ser Pro Pro Lys Gln Ala Glu Ala Val Leu Lys Thr Leu
20 25 30

Gln Glu Leu Lys Lys Leu Thr Ile Ser Glu Gln Asn Ile Gln Arg Ala
35 40 45

Asn Leu Phe Asn Lys Leu Val Thr Glu Leu Arg Gly Leu Ser Asp Glu
50 55 60

Ala Val Thr Ser Leu Leu Pro Gln Leu Ile Glu Val Ser Ser Pro Ile
65 70 75 80

Thr Leu Gln Ala Leu Val Gln Cys Gly Gln Pro Cys Ser Thr His Ile
85 90 95

Leu Gln Trp Leu Lys Arg Val His Ala Asn
100 105

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Trp Phe His Gly Lys Ile Ser Lys Gln Glu Ala Tyr Asn Leu Leu Met
1 5 10 15

Thr Val Gly Gln Ala Cys Ser Phe Leu Val Arg Pro Ser Asp Asn Thr
20 25 30

Pro Gly Asp Tyr Ser Leu Tyr Phe Arg Thr Ser Glu Asn Ile Gln Arg
35 40 45

Phe Lys Ile Cys Pro Thr Pro Asn Asn Gln Phe Met Met Gly Gly Arg
50 55 60

Tyr Tyr Asn Ser Ser Ile Gly Asp Ile Ile Asp His Tyr Arg Lys Glu
65 70 75 80

Gln Ile Val Glu Gly Tyr Tyr Leu Lys Glu Pro
85 90

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ile	Met	Leu	Ser	Val	Glu	Lys	Leu	Ile	Lys	Asp	Leu	Lys	Ser	Lys	Glu
1				5				10					15		
Val	Pro	Glu	Ala	Arg	Ala	Tyr	Leu	Arg	Ile	Leu	Gly	Glu	Glu	Leu	Gly
	20					25						30			
Phe	Ala	Ser	Leu	His	Asp	Leu	Gln	Leu	Leu	Gly	Lys	Leu	Leu	Leu	Met
	35				40						45				
Gly	Ala	Arg	Thr	Leu	Gln	Gly	Ile	Pro	Gln	Met	Ile	Gly	Glu	Val	Ile
	50				55					60					
Arg	Lys	Gly	Ser	Lys	Asn	Asp	Phe	Phe	Leu	His	Tyr	Ile	Phe	Met	Glu
	65				70				75			80			
Asn	Ala	Phe	Glu	Leu	Pro	Thr	Gly	Ala	Gly	Leu	Gln	Leu			
		85				90									

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Trp	Phe	His	Gly	Lys	Ile	Ser	Lys	Gln	Glu	Ala	Tyr	Asn	Leu	Leu	Met
1					5			10				15			
Thr	Val	Gly	Gln	Ala	Cys	Ser	Phe	Leu	Val	Arg	Pro	Ser	Asp	Asn	Thr
	20					25					30				
Pro	Gly	Asp	Tyr	Ser	Leu	Tyr	Phe	Arg	Thr	Ser	Glu	Asn	Ile	Gln	Arg
	35					40					45				
Phe	Lys	Ile	Cys	Pro	Thr	Pro	Asn	Asn	Gln	Phe	Met	Met	Gly	Gly	Arg
	50					55				60					
Tyr	Tyr	Asn	Ser	Ser	Ile	Gly	Asp	Ile	Ile	Asp	His	Tyr	Arg	Lys	Glu
	65					70			75			80			

Gln Ile Val Glu Gly Tyr Tyr Leu Lys
85

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Tyr Phe His Lys Leu Asn Ile Pro Lys Leu Asp Phe Ser Ser Gln Ala
1 5 10 15

Asp Leu Arg Asn Glu Ile Lys Thr Leu Leu Lys Ala Gly His Ile Ala
20 25 30

Trp Thr Ser Ser Gly Lys Gly Ser Trp Lys Trp Ala Cys Pro Arg Phe
35 40 45

Ser Asp Glu Gly Thr His Glu Ser Gln Ile Ser Phe Thr Ile Glu Gly
50 55 60

Pro Leu Thr Ser Phe Gly Leu Ser Asn Lys Ile Asn Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg
1 5 10 15

Asp Thr Pro Asp Gly Thr Phe Leu Val Arg Asp Ala Ser Ser Lys Ile
20 25 30

Gln Gly Asp Tyr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile
35 40 45

Lys Val Phe His Arg Asp Gly Lys Tyr Gly Phe Ser Glu Pro Leu Thr
50 55 60

Phe Cys Ser Val Val Asp Leu Ile Thr His Tyr Arg His Glu Ser Leu
65 70 75 80

Ala Gln Tyr Asn Ala Lys Leu Asp Thr Arg Leu Leu Tyr Pro Val Ser
85 90 95

Lys Tyr

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr Ala Ser Thr Asn Asn Glu
1 5 10 15

Gly Asn Leu Lys Val Arg Phe Pro Leu Arg Leu Thr Gly Lys Ile Asp
20 25 30

Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser Pro Ser Ala Gln Gln Ala
35 40 45

Ser Trp Gln Val Ser Ala Arg Phe Asn Gln Tyr Lys Tyr Asn Gln Asn
50 55 60

Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His Val Gly Ile
65 70 75 80

Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile Pro Leu Thr Ile Pro
85 90 95

Glu Met Arg Leu
100

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Trp Phe His Gly Lys Leu Gly Ala Gly Arg Asp Gly Arg His Ile Ala
1 5 10 15

Glu	Arg	Leu	Leu	Thr	Glu	Tyr	Cys	Ile	Glu	Thr	Gly	Ala	Pro	Asp	Gly
20									25					30	
Ser	Phe	Leu	Val	Arg	Glu	Ser	Glu	Thr	Phe	Val	Gly	Asp	Tyr	Thr	Leu
35									40					45	
Ser	Phe	Trp	Arg	Asn	Gly	Lys	Val	Gln	His	Cys	Arg	Ile	His	Ser	Arg
50									55					60	
Gln	Asp	Ala	Gly	Thr	Pro	Lys	Phe	Phe	Leu	Thr	Asp	Asn	Leu	Val	Phe
65									70			75		80	
Asp	Ser	Leu	Tyr	Asp	Leu	Ile	Thr	His	Tyr	Gln	Gln	Val	Pro	Leu	Arg
									85			90		95	
Cys	Asn	Glu	Phe	Glu	Met	Arg	Leu	Ser	Glu						
					100				105						

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Phe	Pro	Gly	Lys	Pro	Gly	Ile	Tyr	Thr	Arg	Glu	Glu	Leu	Cys	Thr	Met
1						5			10				15		
Phe	Ile	Arg	Glu	Val	Gly	Thr	Val	Leu	Ser	Gln	Val	Tyr	Ser	Lys	Val
						20			25				30		
His	Asn	Gly	Ser	Glu	Ile	Leu	Phe	Ser	Tyr	Phe	Gln	Asp	Leu	Val	Ile
						35			40				45		
Thr	Leu	Pro	Phe	Glu	Leu	Arg	Lys	His	Lys	Leu	Ile	Asp	Val	Ile	Ser
						50			55			60			
Met	Tyr	Arg	Glu	Leu	Leu	Lys	Asp	Leu	Ser	Lys	Glu	Ala	Gln	Glu	Val
65						70				75			80		
Phe	Lys	Ala	Ile	Gln	Ser	Leu	Lys	Thr	Thr	Glu					
						85			90						

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val Ser Asp Gly Ile Ala Ala Leu Asp Leu Asn Ala Val Ala Asn Lys
1 5 10 15

Ile Ala Asp Phe Glu Leu Pro Thr Ile Ile Val Pro Glu Gln Thr Ile
20 25 30

Glu Ile Pro Ser Ile Lys Phe Ser Val Pro Ala Gly Ile Val Ile Pro
35 40 45

Ser Phe Gln Ala Leu Thr Ala Arg Phe Glu Val Asp Ser Pro Val Tyr
50 55 60

Asn Ala Thr Trp Ser Ala Ser Leu Lys Asn Lys Ala Asp Tyr Val Glu
65 70 75 80

Thr Val Leu Asp Ser Thr Cys Ser Ser Thr Val Gln Phe Leu Glu Tyr
85 90 95

Glu Leu Asn Val Leu Gly Thr His Lys Ile Glu Asp Gly Thr Leu Ala
100 105 110

Ser Lys Thr Lys Gly Thr Leu Ala His Arg Asp Phe Ser Ala Glu Tyr
115 120 125

Glu Glu Asp Gly Lys Phe Glu Gly Leu Gln Glu Trp Glu Gly Lys Ala
130 135 140

His Leu Asn Ile Lys Ser Pro Ala Phe Thr Asp Leu His Leu Arg Tyr
145 150 155 160

Gln Lys Asp Lys Lys Gly Ile Ser Thr Ser Ala Ala Ser Pro Ala Val
165 170 175

Gly Thr Val Gly Met Asp Met Asp Glu Asp Asp Asp Phe Ser Lys Trp
180 185 190

Asn Phe Tyr Tyr Ser Pro Gln Ser Ser Pro Asp
195 200

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly
1 5 10 15

Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro
20 25 30

Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu
35 40 45

Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile
50 55 60

Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly
65 70 75 80

Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala
85 90 95

Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His
100 105 110

Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys
115 120 125

Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
130 135 140

Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
145 150 155 160

Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
165 170 175

Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro
180 185 190

Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg
195 200 205

Met Pro Cys Pro Pro Glu
210

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly
1 5 10 15

Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro
20 25 30

Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys Leu Lys His Asp
35 40 45

Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile
50 55 60

Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp Phe Leu Lys Asp
65 70 75 80

Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val Asp Met Ala Ala
85 90 95

Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His
100 105 110

Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn Gly Leu Ile Cys
115 120 125

Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
130 135 140

Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
145 150 155 160

Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
165 170 175

Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr Pro
180 185 190

Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg Gly Tyr Arg
195 200 205

Met Pro Cys Pro Gln
210

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala Thr Tyr Asn Lys
1 5 10 15

His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly Ser Met Ser Val
20 25 30

Glu Ala Phe Leu Ala Glu Ala Asn Val Met Lys Thr Leu Gln His Asp
35 40 45

Lys Leu Val Lys Leu His Ala Val Val Thr Lys Glu Pro Ile Tyr Ile
50 55 60

Ile Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser
65 70 75 80

Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala
85 90 95

Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Gln Arg Asn Tyr Ile His
100 105 110

Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala Ser Leu Val Cys
115 120 125

Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr
130 135 140

Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
145 150 155 160

Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
165 170 175

Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro
180 185 190

Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg
195 200 205

Met Pro Arg Pro Glu
210

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn
1 5 10 15

Ser Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val
20 25 30

Gln Ala Phe Leu Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp
35 40 45

Lys Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr
50 55 60

Ile Ile Thr Glu Tyr Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys
65 70 75 80

Ser Asp Glu Gly Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser
85 90 95

Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile
100 105 110

His Arg Asp Leu Arg Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met
115 120 125

Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu
130 135 140

Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro
145 150 155 160

Glu Ala Ile Asn Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser
165 170 175

Phe Gly Ile Leu Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr
180 185 190

Pro Gly Arg Thr Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr
195 200 205

Arg Met Pro Arg Val Glu Asn Cys Pro Asp
210 215

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly
1 5 10 15

His Thr Lys Val Ala Val Lys Ser Leu Lys Gln Gly Ser Met Ser Pro
20 25 30

Asp Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Gln Leu Gln His Gln
35 40 45

Arg Leu Val Arg Leu Tyr Ala Val Val Thr Gln Glu Pro Ile Tyr Ile
50 55 60

Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Val Asp Phe Leu Lys Thr
65 70 75 80

Pro Ser Gly Ile Lys Leu Thr Ile Asn Lys Leu Leu Asp Met Ala Ala
85 90 95

Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Glu Arg Asn Tyr Ile His
100 105 110

Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Asp Thr Leu Ser Cys
115 120 125

Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
130 135 140

Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
145 150 155 160

Ala Ile Asn Tyr Gly Thr Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
165 170 175

Gly Ile Leu Leu Thr Glu Ile Val Thr His Gly Arg Ile Pro Tyr Pro
180 185 190

Gly Met Thr Asn Pro Glu Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg
195 200 205

Met Val Arg Pro Asp
210

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg Lys Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Gly Thr Leu Ala His Arg Asp Phe Ser Ala Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Asp Leu Asn Ala Val Ala Asn Lys Ile Ala Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Thr Ser Leu Arg Ala Pro Thr Met Pro Pro Pro Leu Pro Pro Val Pro
1 5 10 15

Pro Gln Pro Ala Arg Arg Gln Ser Arg Arg Leu Pro Ala Ser Pro Val
20 25 30

Ile Ser

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro Thr Val Thr Pro Val
1 5 10 15

Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg Pro
20 25 30

Gly Val Gln Glu
35

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro Thr Ile Thr Pro Ile
1 5 10 15

Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg Pro
20 25 30

Gly Val Gln Glu
35

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Asp Ala Glu Trp Thr Ala Phe Val Pro Pro Asn Val Ile Leu Ala
1 5 10 15

Pro Ser Leu Glu Ala Phe Phe Glu Gln Ala Leu Thr Glu Glu Thr Pro
20 25 30

Gly Val Gln Asp
35

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Leu Val Thr Glu Ser Ser Val Leu Ala Thr Leu Thr Val Val Pro Asp
1 5 10 15

Pro Ser Thr Glu Ala Ser Ser Glu Glu Ala Pro Thr Glu Gln Ser Pro
20 25 30

Gly Val Gln Asp
35

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Pro Val Met Glu Ser Thr Leu Leu Thr Thr Pro Thr Val Val Pro Val
1 5 10 15

Pro Ser Thr Glu Leu Pro Ser Glu Glu Ala Pro Thr Glu Asn Ser Thr
20 25 30

Gly Val Gln Asp
35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Pro Val Thr Glu Ser Ser Val Leu Thr Thr Pro Thr Val Ala Pro Val
1 5 10 15

Pro Ser Thr Glu Ala Pro Ser Glu Gln Ala Pro Pro Glu Lys Ser Pro
20 25 30

Val Val Gln Asp
35

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ser Glu Thr Glu Ser Gly Val Leu Glu Thr Pro Thr Val Val Pro Glu
1 5 10 15

Pro Ser Met Glu Ala His Ser Glu Ala Ala Pro Thr Glu Gln Thr Pro
20 25 30

Val Val Arg Arg Gln
35

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Pro Lys Asp Ala Thr Arg Phe Lys His Leu Arg Lys Tyr Thr Tyr Asn
1 5 10 15

Tyr Glu Ala Glu Ser Ser Gly Val Pro Gly Thr Ala Asp Ser Arg
20 25 30

Ser Ala Thr Arg Ile
35

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Pro Lys Asp Ala Thr Arg Phe Lys His Leu Arg Lys Tyr Thr Tyr Asn
1 5 10 15

Tyr Glu Ala Glu Ser Ser Gly Val Pro Gly Thr Ala Asp Ser Arg
20 25 30

Ser Ala Thr Arg Ile
35

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Pro Lys Asp Ala Ser Gln Arg Arg Arg Ser Leu Glu Pro Ala Glu Asn
1 5 10 15

Val His Gly Ala Gly Gly Ala Phe Pro Ala Ser Gln Thr Pro Ser
20 25 30

Lys Pro

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asp Lys Glu Ala Thr Lys Leu Thr Glu Glu Arg Asp Gly Ser Leu Asn
1 5 10 15

Gln Ser Ser Gly Tyr Arg Tyr Gly Thr Asp Pro Thr Pro Gln His Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ile Gln Asn Tyr His Thr Phe Leu Ile Tyr Ile Thr Glu Leu Leu Lys
1 5 10 15

Lys Leu Gln Ser Thr Thr Val Met Asn Pro Tyr Met Lys Leu Ala Pro
20 25 30

Gly Glu Leu Thr Ile Ile Leu
35

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ala	Phe	Leu	Glu	Asp
1				5					10					15	
Tyr	Phe	Thr	Ser	Thr	Glu	Pro	Gln	Tyr	Gln	Pro	Gly	Glu	Asn	Leu	
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu	Glu	Asp
1				5					10					15	
Tyr	Phe	Thr	Ala	Thr	Glu	Pro	Gln	Tyr	Gln	Pro	Gly	Glu	Asn	Leu	
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Val	Leu	Asp	Asp
1				5					10					15	
Phe	Tyr	Thr	Ala	Thr	Glu	Ser	Gln	Tyr	Gln	Gln	Gln	Pro			
		20						25							

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu Asp Asp
1 5 10 15

Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro
20 25

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
1 5 10 15

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
20 25

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Pro Xaa Xaa Xaa Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Pro Asp Phe Arg Leu Pro Glu Ile Ala Ile Pro Glu Phe Ile Ile Pro
1 5 10 15

Thr Leu Asn Leu Asn Asp Phe Gln Val Pro Asp Leu His Ile Pro Glu
20 25 30

Phe Gln Leu Pro His Ile Ser His
35 40

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Pro Gln Asn Ala Lys Leu Lys Ile Lys Arg Pro Val Lys Val Gln Pro
1 5 10 15

Ile Ala Arg Val Trp Tyr
20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Asp Phe Arg Leu Pro Glu Ile Ala Ile Pro Glu Phe Ile Ile Pro
1 5 10 15

Thr Leu Asn Leu Asn Asp
20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asn Asp Phe Gln Val Pro Asp Leu His Ile Pro Glu Phe Gln Leu Pro
1 5 10 15

His Ile Ser His Thr Ile
20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Pro Ser Leu Glu Leu Pro Val Leu His Val Pro Arg Asn Leu Lys Leu
1 5 10 15

Ser Leu Pro His Phe Lys
20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met Ala Ser Gly Arg Ala Arg Cys Thr Arg Lys Leu Arg Asn Trp Val
1 5 10 15

Val Glu Gln Val Glu Ser Gly Gln Phe Pro Gly Val Cys Trp Asp Asp
20 25 30

Thr Ala Lys Thr Met Phe Arg Ile Pro Trp Lys His Ala Gly Lys Gln
35 40 45

Asp Phe Arg Glu Ser Gln Asp Ala Ala Phe Phe Lys Ala Trp Ala Ile
50 55 60

Phe Lys Gly Lys Tyr Lys Glu Gly Asp Lys Glu Val Pro Glu Arg Gly
65 70 75 80

Arg Met Asp Val Ala Glu Pro Tyr Lys Val Tyr Gln Leu Leu Pro Pro
85 90 95

Gly Ile Val Ser Gly Gln Pro Gly Thr Gln Lys Val Pro Ser Lys Arg
100 105 110

Gln His Ser Ser Val Ser Ser Glu Arg Lys Glu Glu Asp Ala Met Gln
115 120 125

Asn Cys Thr Leu Ser Pro Ser Val Leu Gln Asp Ser Leu Asn Asn Glu
 130 135 140
 Glu Gly Ala Ser Gly Gly Ala Val His Ser Asp Ile Gly Ser Ser Ser
 145 150 155 160
 Ser Ser Ser Pro Glu Pro Gln Glu Val Thr Asp Thr Thr Glu Ala
 165 170 175
 Pro Phe Gln Gly Asp Gln Arg Ser Leu Glu Phe Leu Leu Pro Pro Glu
 180 185 190
 Pro Asp Tyr Ser Leu Leu Leu Thr Phe Ile Tyr Asn Gly Arg Val Val
 195 200 205
 Gly Glu Ala Gln Val Gln Ser Leu Asp Cys Arg Leu Val Ala Glu Pro
 210 215 220
 Ser Gly Ser Glu Ser Ser Met Glu Gln Val Leu Phe Pro Lys Pro Gly
 225 230 235 240
 Pro Glu Pro Thr Gln Arg Leu Leu Ser Gln Leu Glu Arg Gly Ile Leu
 245 250 255
 Val Ala Ser Asn Pro Arg Gly Leu Phe Val Gln Arg Leu Cys Pro Ile
 260 265 270
 Pro Ile Ser Trp Asn Ala Pro Gln Ala Pro Pro Gly Pro Gly Pro His
 275 280 285
 Leu Leu Pro Ser Asn Glu Cys Val Glu Leu Phe Arg Thr Ala Tyr Phe
 290 295 300
 Cys Arg Asp Leu Val Arg Tyr Phe Gln Gly Leu Gly Pro Pro Pro Lys
 305 310 315 320
 Phe Gln Val Thr Leu Asn Phe Trp Glu Glu Ser His Gly Ser Ser His
 325 330 335
 Thr Pro Gln Asn Leu Ile Thr Val Lys Met Glu Gln Ala Phe Ala Arg
 340 345 350
 Tyr Leu Lys Met Glu Gln Ala Phe Ala Arg Tyr Leu Leu Glu Gln Thr
 355 360 365
 Pro Glu Gln Gln Ala Ala Ile Leu Ser Leu Val
 370 375

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Val Ser Leu Val Cys Pro Lys Asp Ala Thr Arg Phe Lys His Leu Arg
1 5 10 15

Lys Tyr Thr Tyr Asn Tyr Glu Ala Glu Ser Ser Ser Gly Val Pro Gly
20 25 30

Thr Ala Asp Ser Arg Ser Ala Thr Arg Ile Asn Cys Lys Val Glu Leu
35 40 45

Glu Val Pro Gln Leu Cys Ser Phe Ile Leu Lys Thr Ser Gln Cys Thr
50 55 60

Leu Lys Glu Val Tyr Gly Phe Asn Pro Glu Gly Lys Ala Leu Leu Lys
65 70 75 80

Lys Thr Lys Asn Ser Glu Glu Phe Ala Ala Ala Met Ser Arg Tyr Glu
85 90 95

Leu Lys Leu Ala Ile Pro Glu Gly Lys Gln Val Phe Leu Tyr Pro Glu
100 105 110

Lys Asp Glu Pro Thr Tyr Ile Leu Asn Ile Lys Arg Gly Ile Ile Ser
115 120 125

Ala Leu Leu Val Pro Pro Glu Thr Glu Glu Ala Lys Gln Val Leu Phe
130 135 140

Leu Asp Thr Val Tyr Gly Asn Cys Ser Thr His Phe Thr Val Lys Thr
145 150 155 160

Arg Lys Gly Asn Val Ala Thr Glu Ile Ser Thr Glu Arg Asp Leu Gly
165 170 175

Gln Cys Asp Arg Phe Lys Pro Ile Arg Thr Gly Ile Ser Pro Leu Ala
180 185 190

Leu Ile Lys Gly Met Thr Arg Pro Leu Ser Thr Leu Ile Ser Ser Ser
195 200 205

Gln Ser Cys Gln Tyr Thr Leu Asp Ala Lys Arg Lys His Val Ala Glu
210 215 220

Ala Ile Cys Lys Glu Gln His Leu Phe Leu Pro Phe Ser Tyr Lys Asn
225 230 235 240

Lys Tyr Gly Met Val Ala Gln Val Thr Gln Thr Leu Lys Leu Glu Asp
245 250 255

Thr Pro Lys Ile Asn Ser Arg Phe Phe Gly Glu Gly Thr Lys Lys Met
 260 265 270
 Gly Leu Ala Phe Glu Ser Thr Lys Ser Thr Ser Pro Pro Lys Gln Ala
 275 280 285
 Glu Ala Val Leu Lys Thr Leu Gln Glu Leu Lys Lys Leu Thr Ile Ser
 290 295 300
 Glu Gln Asn Ile Gln Arg Ala Asn Leu Phe Asn Lys Leu Val Thr Glu
 305 310 315 320
 Leu Arg Gly Leu Ser Asp Glu Ala Val Thr Ser Leu Leu Pro Gln Leu
 325 330 335
 Ile Glu Val Ser Ser Pro Ile Thr Leu Gln Ala Leu Val Gln Cys Gly
 340 345 350
 Gln Pro Gln Cys Ser Thr His Ile Leu Lys Arg Val His Ala Asn Pro
 355 360 365
 Leu Leu Ile Asp Val Val Thr Tyr Leu Val Ala Leu Ile Pro Glu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Gly Leu Ser Asn Lys Ile Asn Ser Lys His Leu Arg Val Asn Gln
 1 5 10 15
 Asn Leu Val Tyr Glu Ser Gly Ser Leu Asn Phe Ser Lys Leu Glu Ile
 20 25 30
 Gln Ser Gln Val Asp Ser Gln His Val Gly His Ser Val Leu Thr Ala
 35 40 45
 Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala Glu Phe Thr Gly Arg
 50 55 60
 His Asp Ala His Leu Asn Gly Lys Val Ile Gly Thr Leu Lys Asn Ser
 65 70 75 80
 Leu Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr Ala Ser Thr Asn Asn
 85 90 95

Glu Gly Asn Leu Lys Val Arg Phe Pro Leu Arg Leu Thr Gly Lys Ile
100 105 110

Asp Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser Pro Ser Ala Gln Gln
115 120 125

Ala Ser Trp Gln Val Ser Ala Arg Phe Asn Gln Tyr Lys Tyr Asn Gln
130 135 140

Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His Val Gly
145 150 155 160

Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile Pro Leu Thr Ile
165 170 175

Pro Glu Met Arg Leu Pro Tyr Thr Ile Ile Thr Thr Pro Pro Leu Lys
180 185 190

Asp Phe Ser Leu Trp Glu Lys Thr Gly Leu Lys Glu Phe Leu Lys Thr
195 200 205

Thr Lys Gln Ser Phe Asp Leu Ser Val Lys Ala Gln Tyr Lys Lys Asn
210 215 220 240

Lys His Arg His Ser Ile Asn Pro Leu Ala Val Leu Cys Glu Phe Ile
225 230 235 240

Ser Gln Ser Ile Lys Ser Phe Asp Arg His Phe Glu Lys Asn Arg Asn
245 250 255

Asn Ala Leu Asp Phe Val Thr Lys Ser Tyr Asn Glu Thr Lys Ile Lys
260 265 270

Phe Asp Lys Tyr Lys Ala Glu Lys Ser His Asp Glu Leu Pro Arg Thr
275 280 285

Phe Gln Ile Pro Gly Tyr Thr Val Pro Val Val Asn Val Glu Val Ser
290 295 300

Pro Phe Thr Ile Glu Met Ser Ala Phe Gly Tyr Val Phe Pro Lys Ala
305 310 315 320

Val Ser Met Pro Ser Phe Ser Ile Leu Gly Ser Asp Val Arg Val Pro
325 330 335

Ser Tyr Thr Leu Ile Leu Pro Ser Leu Glu Leu Pro Val Leu His Val
340 345 350

Pro Arg Asn Leu Lys Leu Ser Leu Pro His Phe Lys Glu Leu Cys Thr
355 360 365

Ile Ser His Ile Phe Ile Pro Ala Met Gly Asn Ile Thr Tyr Asp Phe
370 375 380

Ser Phe Lys Ser Ser Val Ile Thr Leu Asn
385 390

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ala Ser Gly Arg Ala Arg Cys Thr Arg Lys Leu Arg Asn Trp Val
1 5 10 15

Val Glu Gln Val Glu Ser Gly Gln Phe Pro Gly Val Cys Trp Asp Asp
20 25 30

Thr Ala Lys Thr Met Phe Arg Ile Pro Trp Lys His Ala Gly Lys Gln
35 40 45

Asp Phe Arg
50

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Pro Lys Asp Ala Thr Arg Phe Lys His Leu Arg Lys Tyr Thr Tyr Asn
1 5 10 15

Tyr Glu Ala Glu Ser Ser Gly Val Pro Gly Thr Ala Asp Ser Arg
20 25 30

Ser Ala Thr Arg Ile Asn Cys Lys Val Glu Leu Glu Val Leu Pro Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Pro Glu Gly Lys Ala Leu Leu Lys Lys Thr Lys Asn Ser Glu Glu Phe
1 5 10 15
Ala Ala Ala Met Ser Arg Tyr Glu Leu Lys Leu Ala Ile Pro Glu Gly
20 25 30
Lys Gln Val Phe Leu
35

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Cys Ser Thr His Phe Thr Val Lys Thr Arg Lys Gly Asn Val Ala Thr
1 5 10 15
Glu Ile Ser Thr Glu Arg Asp Leu Gly Gln Cys Asp Arg Phe Lys Pro
20 25 30
Ile Arg Thr Gly Ile Ser
35

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Cys Ser Thr His Ile Leu Gln Trp Leu Lys Arg Val His Ala Asn Pro
1 5 10 15
Leu Leu Ile Asp Val Val Thr Tyr Leu Val Ala Leu Ile Pro Glu Pro
20 25 30
Ser Ala Gln Gln Leu Arg Glu Ile Phe Asn Met Ala Arg Asp Gln Arg
35 40 45
Ser Arg Ala
50

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

His	Leu	Ser	Cys	Asp	Thr	Lys	Glu	Glu	Arg	Lys	Ile	Lys	Gly	Val	Ile
1						5				10					15
Ser	Ile	Pro	Arg	Leu	Gln	Ala	Glu	Ala	Arg	Ser	Glu	Ile	Leu	Ala	His
				20				25					30		
Trp	Ser	Pro	Ala	Lys	Leu										
				35											

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ser	Val	His	Leu	Asp	Ser	Lys	Lys	Gln	His	Leu	Phe	Val	Lys	Glu	
1						5				10				15	
Val	Lys	Ile	Asp	Gly	Gln	Phe	Arg	Val	Ser	Ser	Phe	Tyr	Ala	Lys	Gly
		20						25				30			
Thr	Tyr	Gly	Leu	Ser	Cys	Gln	Arg	Asp	Pro	Asn	Thr	Gly	Arg	Leu	
			35					40			45				

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Lys	His	Ile	Asn	Ile	Asp	Gln	Phe	Val	Arg	Lys	Tyr	Arg	Ala	Ala	Leu
1						5			10						15

Gly Lys Leu Pro Gln Gln Ala Asn Asp Tyr Leu Ser Phe Asn Trp Glu
20 25 30

Arg Gln Val Ser His Ala Lys Glu
35 40

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Lys Leu Thr Ala Leu Thr Lys Lys Tyr Arg Ile Thr Glu Asn Asp Ile
1 5 10 15

Gln Ile Ala Leu Asp Asp Ala Lys Ile Asn Phe Asn Glu Lys Leu Ser
20 25 30

Gln Leu Gln Thr Tyr Met Ile Gln
35 40

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu Arg Ile Asn Asp Val Leu Glu His Val Lys His Phe Val Ile Asn
1 5 10 15

Leu Ile Gly Asp Phe Glu Val Ala Glu Lys Ile Asn Ala Phe Arg Ala
20 25 30

Lys Val His Glu Leu Ile Glu Arg Tyr Glu Val Asp Gln Gln Ile Gln
35 40 45

Val Leu
50

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asn Lys Phe Leu Asp Met Leu Ile Lys Lys Leu Lys Ser Phe Asp Tyr
1 5 10 15

His Gln Phe Val Asp Glu Thr Asn Asp Lys Ile Arg Glu Val Thr Gln
20 25 30

Arg Leu Asn Gly Glu Ile Gln Ala Leu Glu Leu Pro Gln Lys Ala Glu
35 40 45

Ala Leu
50

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ser Asn Lys Ile Asn Ser Lys His Leu Arg Val Asn Gln Asn Leu Val
1 5 10 15

Tyr Glu Ser Gly Ser Leu Asn
20

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Phe Ser Lys Leu Glu Ile Gln Ser Gln Val Asp Ser Gln His Val Gly
1 5 10 15

His Ser Val Leu Thr Ala Lys Gly Met Ala Leu Phe Gly Glu Gly Gly
20 25 30

Lys Ala Glu Phe Thr Gly Arg His Asp Ala His Leu Asn Gly Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Val Lys Ala Gln Tyr Lys Lys Asn Lys His Arg His Ser Ile Thr Asn
1 5 10 15

Pro Leu Ala Val Leu Cys Glu Phe Ile Ser Gln Ser Ile Lys Ser Phe
20 25 30

Asp Arg His Phe Glu Lys Asn Arg Asn Asn Ala Leu Asp Phe Val Thr
35 40 45

Lys Ser
50

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Leu Glu Gly Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys Leu
1 5 10 15

Ala Thr Ala Leu Ser Leu Ser Asn Lys Phe Val Glu Gly Ser His Asn
20 25 30

Ser Thr Val Ser Leu Thr Thr Lys Asn Met Glu Val Ser Val Ala Lys
35 40 45

Thr Thr Lys
50

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Lys Leu Asp Val Thr Thr Ser Ile Gly Arg Arg Gln His Leu Arg Val
1 5 10 15

Ser Thr Ala Phe Val Tyr Thr Lys Asn Pro Asn Gly Tyr Ser Phe Ser
20 25 30

Ile Pro Val Lys Val Leu Ala Asp Lys Phe Ile Thr Pro Gly Leu Lys
35 40 45

Leu Asn Asp
50

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Phe Arg Glu Ile Gln Ile Tyr Lys Lys Leu Arg Thr Ser Ser Phe Ala
1 5 10 15

Leu Asn Leu Pro Thr Leu Pro Glu Val Lys Phe Pro Glu Val Asp Val
20 25 30

Leu Thr Lys Tyr Ser Gln Pro Glu Asp Ser Leu Ile Pro Phe Phe Glu
35 40 45

Ile

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Leu His Leu Arg Tyr Gln Lys Asp Lys Lys Gly Ile Ser Thr Ser Ala
1 5 10 15

Ala Ser Pro Ala Val Gly Thr Val Gly Met Asp Met Asp Glu Asp Asp
20 25 30

Asp Phe Ser Lys Trp Asn Phe Tyr Tyr Ser Pro Gln Ser Ser Pro Asp
35 40 45

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu Arg Glu Val Ser Ser Lys Leu Arg Arg Asn Leu Gln Asn Asn Ala
1 5 10 15

Glu Trp Val Tyr Gln Gly Ala Ile Arg Gln Ile Asp Asp Ile Asp Val
20 25 30

Arg Phe Gln Lys Ala Ala Ser Gly Thr Thr Gly Thr Tyr Gln Glu Trp
35 40 45

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Arg Val Thr Gln Lys Phe His Met Lys Val Lys His Leu Ile Asp Ser
1 5 10 15

Leu Ile Asp Phe Leu Asn Phe Pro Arg Phe Gln Phe Pro Gly Lys Pro
20 25 30

Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met Phe Ile Arg Glu Val
35 40 45

Gly Thr
50

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp Lys His Ala Gly Lys Gln Asp Phe Arg Glu Ser Gln Asp Ala Ala
1 5 10 15

Ala Phe Phe Lys Ala Trp Ala Ile Phe Lys Gly Lys Tyr Lys Glu Gly
20 25 30

Asp Lys Glu Val Pro Glu Arg Gly Arg Met Asp Val Ala Glu Pro Tyr
35 40 45

Lys

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Glu His Val Lys His Phe Val Ile Asn Leu Ile Gly Asp Phe Glu Val
1 5 10 15

Ala Glu Lys Ile Asn Ala Phe Arg Ala Lys Val His Glu Leu Ile Glu
20 25 30

Arg Tyr Glu Val Asp Gln Gln Ile Gln Val Leu Met Asp Lys Leu Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Val Arg Lys Tyr Arg Ala Ala Leu Gly Lys Leu Pro Gln Gln Ala Asn
1 5 10 15

Asp Tyr Leu Asn Ser Phe Asn Trp Glu Arg Gln Val Ser His Ala Lys
20 25 30

Glu Lys Leu Thr Ala Leu Thr Lys Lys Tyr Arg Ile Thr Glu Asn Asp
35 40 45

Ile Gln Ile Ala
50

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Tyr Ile Lys Asp Ser Tyr Asp Leu His Asp Leu Lys Ile Ala Ile Ala
1 5 10 15

Asn Ile Ile Asp Glu Ile Ile Glu Lys Leu Lys Ser Leu Asp Glu His
20 25 30

Tyr His Ile Arg Val Asn Leu Val Lys Thr Ile His Asp Leu His Leu
35 40 45

Phe Ile Glu Asn Ile Asp Phe Asn Lys
50 55

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Lys Ile Thr Leu Ile Ile Asn Trp Leu Gln Glu Ala Leu Ser Ser Ala
1 5 10 15

Ser Leu Ala His Met Lys Ala Lys Phe Arg Glu Thr Leu Glu Asp Thr
20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Thr Asp His Phe Ser Leu Arg Ala Arg Tyr His Met Lys Ala Asp Ser
1 5 10 15

Val Val Asp Leu Ser Tyr Asn Val Gln Gly Ser Gly Glu Thr Thr Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Lys Leu Thr Thr Asn Gly Arg Phe Arg Glu His Asn Ala Lys Phe Ser
1 5 10 15

Leu Asp Gly Lys
20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Asp Thr Lys Tyr Gln Ile Arg Ile Gln Ile Gln Glu Lys Leu Gln Gln
1 5 10 15

Leu Lys Arg His Ile Gln Asn Ile Asp Ile Gln His Leu Ala Gly Lys
20 25 30

Leu Lys Gln His Ile Glu Ala Ile Asp Val Arg Val Leu Leu Asp Gln
35 40 45

Leu Gly Thr Thr
50

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe His Asp Phe Pro Asp Leu Gly Gln Glu Val Ala Leu Asn Ala Asn
1 5 10 15

Thr Lys Asn Gln Lys Ile Arg Trp Lys Asn Glu Val Arg Ile His Ser
20 25 30

Gly Ser Phe Gln Ser Gln Val Glu Leu Ser Asn Asp Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Lys Asp Asn Val Phe Asp Gly Leu Val Arg Val Thr Gln Lys Phe His
1 5 10 15

Met Lys Val Lys His Leu Ile Asp Ser Leu Ile Asp Phe Leu Asn Phe
20 25 30

Pro Arg

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

His Arg Asn Ile Gln Glu Tyr Leu Ser Ile Leu Thr Asp Pro Asp Gly
1 5 10 15

Lys Gly Lys Glu Lys Ile Ala Glu Leu Ser Ala Thr Ala Gln Glu Ile
20 25 30

Ile Lys Ser
35

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Glu Phe Thr Ile Val Ala Phe Val Lys Tyr Asp Lys Asn Gln Asp Val
1 5 10 15

His Ser Ile Asn Leu Pro Phe Phe Glu Thr Leu Gln Glu Tyr Phe Glu
20 25 30

Arg Asn Arg Gln Thr Ile Val Val Val Glu Asn Val Gln Arg Asn Leu
35 40 45

Lys His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg Ala Ala Leu
50 55 60

Gly Lys Leu Pro Gln Gln Ala Asn Asp Tyr Leu Asn Ser Phe Asn Trp
65 70 75 80

Glu Arg Gln Val Ser His Ala Lys Glu Lys Leu Thr Ala Leu Thr Lys
85 90 95

Lys Tyr Arg Ile Thr Glu Asn Asp Ile Gln Ile Ala Leu Asp Asp Ala
100 105 110

Lys Ile Asn Phe Asn Glu Lys Leu Ser Gln Leu Gln Thr Tyr Met Ile
115 120 125

Gln Phe Asp Gln Tyr Ile Lys Asp Ser Tyr Asp Leu His Asp Leu Lys
130 135 140

Ile Ala Ile Ala Asn Ile Ile Asp Glu Ile Ile Glu Lys Leu Lys Ser
145 150 155 160

Leu Asp Glu His Tyr His Ile Arg Val Asn Leu Val Lys Thr Ile His
165 170 175

Asp	Leu	His	Leu	Phe	Ile	Glu	Asn	Ile	Asp	Phe	Asn	Lys	Ser	Gly	Ser
180									185						190
Ser	Thr	Ala	Ser	Trp	Ile	Gln	Asn	Val	Asp	Thr	Lys	Tyr	Gln	Ile	Arg
195									200						205
Ile	Gln														
210															

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gly	Pro	Leu	Pro	Thr	Leu	Val	Ser	Gly	Gly	Thr	Ile	Leu	Ala	Thr	Val
1											5				15

Pro	Leu	Val	Val	Asp	Ala	Glu	Lys	Leu	Pro	Ile	Asn	Arg	Leu	Ala	Ala
										20			25		30

Gly	Ser	Lys	Ala	Pro	Ala	Ser	Ala	Gln	Ser	Arg	Gly	Glu	Lys	Arg	Thr
									35		40		45		

Ala	His	Asn	Ala	Ile	Glu	Lys	Arg	Tyr	Arg	Ser	Ser	Ile	Asn	Asp	Lys
									50		55		60		

Ile	Ile	Glu	Leu	Lys	Asp	Leu	Val	Val	Gly	Thr	Glu	Ala	Lys	Leu	Asn
									65		70		75		80

Lys	Ser	Ala	Val	Leu	Arg	Lys	Ala	Ile	Asp	Tyr	Ile	Arg	Phe	Leu	Gln
									85		90		95		

His	Ser	Asn	Gln	Lys	Leu	Lys	Gln	Glu	Asn	Leu	Ser	Leu	Arg	Thr	Ala
									100		105		110		

Val	His	Lys	Ser	Lys	Ser	Leu	Lys	Asp	Leu	Val	Ser	Ala	Cys	Gly	Ser
									115		120		125		

Gly	Gly	Asn	Thr	Asp	Val	Leu	Met	Glu	Gly	Val	Lys	Thr	Glu	Val	Glu
									130		135		140		

Asp	Thr	Leu	Thr	Pro	Pro	Pro	Ser	Asp	Ala	Gly	Ser	Pro	Phe	Gln	Ser
									145		150		155		160

Ser	Pro	Leu	Ser	Leu	Gly	Ser	Arg	Gly	Ser	Gly	Ser	Gly	Gly		
									165		170				

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Gln Val Pro Thr Leu Val Gly Ser Ser Gly Thr Ile Leu Thr Thr Met
1 5 10 15

Pro Val Met Met Gly Gln Glu Lys Val Pro Ile Lys Gln Val Pro Gly
20 25 30

Gly Val Lys Gln Leu Glu Pro Pro Lys Glu Gly Glu Arg Arg Thr Thr
35 40 45

His Asn Ile Ile Glu Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys Ile
50 55 60

Ile Glu Leu Lys Asp Leu Val Met Gly Thr Asp Ala Lys Met His Lys
65 70 75 80

Ser Gly Val Leu Arg Lys Ala Ile Asp Tyr Ile Lys Tyr Leu Gln Gln
85 90 95

Val Asn His Lys Leu Arg Gln Glu Asn Met Val Leu Lys Leu Ala Asn
100 105 110

Gln Lys Asn Lys Leu Leu Lys Gly Ile Asp Leu Gly Ser Leu Val Asp
115 120 125

Asn Glu Val Asp Leu Lys Ile Glu Asp Phe Asn Gln Asn Val Leu Leu
130 135 140

Met Ser Pro Pro Ala Ser Asp Ser Gly Ser Gln Ala Gly Phe Ser Pro
145 150 155 160

Tyr Ser Ile Asp Ser Glu Pro Gly Ser Pro Leu Leu
165 170

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Gly Pro Leu Gln Thr Leu Val Ser Gly Gly Thr Ile Leu Ala Thr Val
1 5 10 15

Pro Leu Val Val Asp Thr Asp Lys Leu Pro Ile His Arg Leu Ala Ala
20 25 30

Gly Gly Lys Ala Leu Gly Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr
35 40 45

Ala His Asn Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys
50 55 60

Ile Val Glu Leu Lys Asp Leu Val Val Gly Thr Glu Ala Lys Leu Asn
65 70 75 80

Lys Ser Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln
85 90 95

His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Thr Leu Arg Ser Ala
100 105 110

His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala Cys Gly Ser Gly
115 120 125

Gly Gly Thr Asp Val Ser Met Glu Gly Met Lys Pro Glu Val Val Glu
130 135 140

Thr Leu Thr Pro Pro Ser Asp Ala Gly Ser Pro Ser Gln Ser Ser
145 150 155 160

Pro Leu Ser Leu Gly Ser Arg Gly Ser Ser Ser Gly Gly
165 170

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr
1 5 10 15

Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
20 25 30

Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp
35 40 45

Asn	Trp	Asp	Ser	Val	Thr	Ser	Thr	Phe	Ser	Lys	Leu	Arg	Glu	Gln	Leu
50															60
Gly	Pro	Val	Thr	Gln	Glu	Phe	Trp	Asp	Asn	Leu	Glu	Lys	Glu	Thr	Glu
65															80
Gly	Leu	Arg	Gln	Glu	Met	Ser	Lys	Asp	Leu	Glu	Glu	Val	Lys	Ala	Lys
															95
85															
Val	Gln	Pro	Tyr	Leu	Asp	Asp	Phe	Gln	Lys	Lys	Trp	Gln	Glu	Glu	Met
															110
100															
Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	Pro	Leu	Arg	Ala	Glu	Leu	Gln	Glu
															125
115															
Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	Leu	Gln	Glu	Lys	Leu	Ser	Pro	Leu
															140
130															
Gly	Glu	Glu	Met	Arg	Asp	Arg	Ala	Arg	Ala	His	Val	Asp	Ala	Leu	Arg
															160
145															
Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	Glu	Leu	Arg	Gln	Arg	Leu	Ala	Ala
															175
165															
Arg	Leu	Glu	Ala	Leu	Lys	Glu	Asn	Gly	Gly	Ala	Arg	Leu	Ala	Glu	Tyr
															190
180															
His	Ala	Lys	Ala	Thr	Glu	His	Leu	Ser	Thr	Leu	Ser	Glu	Lys	Ala	Lys
															205
195															
Pro	Ala	Leu	Glu	Asp	Leu	Arg	Gln	Gly	Leu	Leu	Pro	Val	Leu	Glu	Ser
															220
210															
Phe	Lys	Val	Ser	Phe	Leu	Ser	Ala	Leu	Glu	Glu	Tyr	Thr	Lys	Lys	Leu
															240
225															
Asn	Thr	Gln													

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Gln	Gln	Val	Pro	Val	Leu	Leu	Gln	Pro	His	Phe	Ile	Lys	Ala	Asp	Ser
1															15
5															
10															

Leu Leu Leu Thr Ala Met Lys Thr Asp Gly Ala Thr Val Lys Ala Ala
 20 25 30

Gly Leu Ser Pro Leu Val Ser Gly Thr Thr Val Gln Thr Gly Pro Leu
 35 40 45

Pro Thr Leu Val Ser Gly Gly Thr Ile Leu Ala Thr Val Pro Leu Val
 50 55 60

Val Asp Ala Glu Lys Leu Pro Ile Asn Arg Leu Ala Ala Gly Ser Lys
 65 70 75 80

Ala Pro Ala Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr Ala His Asn
 85 90 95

Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys Ile Ile Glu
 100 105 110

Leu Lys Asp Leu Val Val Gly Thr Glu Ala Lys Leu Asn Lys Ser Ala
 115 120 125

Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln His Ser Asn
 130 135 140

Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu Arg Thr Ala Val His Lys
 145 150 155 160

Ser Lys Ser Leu Lys Asp Leu Val Ser Ala Cys Gly Ser Gly Gly Asn
 165 170 175

Thr Asp Val Leu Met Glu Gly Val Lys Thr Glu Val Glu Asp Thr Leu
 180 185 190

Thr Pro Pro Pro Ser Asp Ala Gly Ser Pro Phe Gln Ser Ser Pro Leu
 195 200 205

Ser Leu Gly Ser Arg Gly Ser Gly Ser Gly Ser Gly Ser Asp Ser
 210 215 220

Glu Pro Asp Ser Pro Val Phe Glu Asp Ser Lys Ala Lys Pro Glu Gln
 225 230 235 240

Arg Pro Ser Leu His Ser Arg Gly Met Leu Asp Arg Ser Arg Leu Leu
 245 250 255

Ala Leu Cys Thr Leu Val Phe Leu Cys Leu Ser Cys Asn
 260 265

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Gln	Ala	Lys	Glu	Pro	Cys	Val	Glu	Ser	Leu	Val	Ser	Gln	Tyr	Phe	Gln
1															15
	5								10						
Thr	Val	Thr	Asp	Tyr	Gly	Lys	Asp	Leu	Met	Glu	Lys	Val	Lys	Ser	Pro
															30
	20							25							
Glu	Leu	Gln	Ala	Glu	Ala	Lys	Ser	Tyr	Phe	Glu	Lys	Ser	Lys	Glu	Gln
															45
	35						40								
Leu	Thr	Pro	Leu	Ile	Lys	Lys	Ala	Gly	Thr	Glu	Leu	Val	Asn	Phe	Leu
															60
	50						55								
Ser	Tyr	Phe	Val	Glu	Leu	Gly	Thr	Gln	Pro	Ala	Thr	Gln			
	65					70					75				

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Glu	Ala	Lys	Leu	Asn	Lys	Ser	Ala	Val	Leu	Arg	Lys	Ala	Ile	Asp	Tyr
1															15
	5									10					
Ile	Arg	Phe	Leu	Gln	His	Ser	Asn	Gln	Lys	Leu	Lys	Gln	Glu	Asn	Leu
															30
	20							25							
Ser	Leu	Arg	Thr	Ala	Val	His	Lys	Ser	Lys	Ser	Leu	Lys	Asp	Leu	Val
															45
	35							40							
Ser	Ala	Cys	Gly	Ser	Gly	Gly	Asn	Thr	Asp	Val	Leu	Met	Glu	Gly	Val
															60
	50						55								
Lys	Thr	Glu	Val	Glu	Asp	Thr									
	65					70									

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gln Lys Ser Glu Leu Thr Gln Gln Leu Asn Ala Leu Phe Gln Asp Lys
1 5 10 15

Leu Gly Glu Val Asn Thr Tyr Ala Gly Asp Leu Gln Lys Lys Leu Val
20 25 30

Pro Phe Ala Thr Glu Leu His Glu Arg Leu Ala Lys Asp Ser Glu Lys
35 40 45

Leu Lys Glu Glu Ile Gly Lys Glu Leu Glu Glu Leu Arg Ala Arg Leu
50 55 60

Leu Pro His Ala Asn Glu Val Ser Gln Lys Ile Gly Asp Asn Leu Arg
65 70 75 80

Glu Leu Gln Gln Arg Leu Glu Pro Tyr Ala Asp Gln Leu Arg Thr Gln
85 90 95

Val Asn Thr Gln Ala Glu Gln Leu Arg Arg Gln Leu Asp Pro Leu Ala
100 105 110

Gln Arg Met Glu Arg Val Leu Arg Glu Asn Ala Asp Ser Leu Gln Ala
115 120 125

Ser Leu Arg Pro His Ala Asp Glu Leu Lys Ala Lys Ile Asp Gln Asn
130 135 140

Val Glu Glu Leu Lys Gly Arg Leu Thr Pro Tyr Ala Asp Glu Phe Lys
145 150 155 160

Val Lys Ile Asp Gln Thr Val Glu Glu Leu Arg Arg Ser Leu Ala Pro
165 170 175

Tyr Ala Gln Asp Thr Gln Glu Lys Leu Asn His Gln Leu Glu Gly Leu
180 185 190

Thr Phe Gln Met Lys Lys Asn Ala Glu Glu Leu Lys Ala Arg Ile Ser
195 200 205

Ala Ser Ala Glu Ile Asp Gln Thr Val Glu Glu Leu Arg Arg Ser Leu
210 215 220

Ala Pro Tyr Ala Gln Asp Thr Gln Glu Lys Leu Asn His Gln Leu Glu
225 230 235 240

Gly Leu Thr Phe Gln Met Lys Lys Asn Ala Glu Glu Leu Lys Ala Arg
245 250 255

Ile Ser Ala Ser Ala Glu Glu Leu Arg Gln Arg Leu Ala Pro Leu Ala
260 265 270

Glu	Asp	Val	Arg	Gly	Asn	Leu	Lys	Gly	Asn	Thr	Glu	Gly	Leu	Gln	Lys
275															285
Ser	Leu	Ala	Glu	Leu	Gly	Gly	His	Leu	Asp	Gln	Gln	Val	Glu	Glu	Phe
290															300
Arg	Arg	Arg	Val	Glu	Pro	Tyr	Gly	Glu	Asn	Phe	Asn	Lys	Ala	Leu	Val
305															320
Gln	Gln	Met	Glu	Gln	Leu	Arg	Gln	Lys	Leu	Gly	Pro	His	Ala	Gly	Asp
															335
325															
Val	Glu	Gly	His	Leu	Ser	Phe	Leu	Glu	Lys	Asp	Leu	Arg	Asp	Lys	Val
															350
340															
Asn	Ser	Phe	Phe	Ser	Thr	Phe	Lys	Glu	Lys	Glu	Ser	Gln	Asp	Lys	Thr
															365
355															
Leu	Ser	Leu	Pro	Glu	Leu	Glu	Gln	Gln	Glu	Gln	Gln	Gln	Glu	Gln	
370															
375															
Gln	Gln	Glu	Gln	Val	Gln	Met	Leu	Ala	Pro	Leu	Glu	Ser			
385															
390															
395															

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Glu	Lys	Leu	Pro	Ile	Asn	Arg	Leu	Ala	Ala	Gly	Ser	Lys	Ala	Pro	Ala
1															15
Ser	Ala	Gln	Ser	Arg	Gly	Glu	Lys	Arg	Thr	Ala	His	Asn	Ala	Ile	Glu
20															30
Lys	Arg	Tyr	Arg	Ser	Ser	Ile	Asn	Asp	Lys	Ile	Ile	Glu	Leu	Lys	Asp
35															45
Leu	Val	Val	Gly	Thr	Glu	Ala	Lys	Leu	Asn	Lys	Ser	Ala	Val	Leu	Arg
50															60
Lys	Ala	Ile	Asp	Tyr	Ile	Arg	Phe	Leu	Gln	His	Ser	Asn	Gln	Lys	Leu
65															80
Lys	Gln	Glu	Asn	Leu	Ser	Leu	Arg	Thr	Ala	Val	His	Lys	Ser	Ser	
85															95

Leu Lys Asp Leu Val Ser Ala Cys Gly Ser Gly Gly Asn Thr Asp Val
100 105 110

Leu Met Glu Gly Val Lys Thr Glu Val Glu Asp Thr Leu Thr Pro Pro
115 120 125

Pro Ser Asp Ala Lys Pro Phe Gln Ser Ser Pro Leu Ser Leu Lys Arg
130 135 140

Lys Lys Gly Lys Lys Asp Ser Glu Pro Asp Ser Pro Val Phe Glu Asp
145 150 155 160

Ser Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg Gly Met
165 170 175

Leu Asp Arg Ser Arg Leu Ala Leu Cys Thr Leu Val Phe Leu Cys Leu
180 185 190

Ser Cys Asn Pro Leu Ala Ser Leu Leu Gly Ala Arg Gly Leu Pro Ser
195 200 205

Pro Ser Asp Thr Thr Ser Val Tyr His Ser Pro Gly Arg Asn Val Leu
210 215 220

Gly Thr Glu Arg Asp Gly Pro Gly Trp Ala Gln Ala Val Gln Leu Phe
225 230 235 240

Leu Cys Asp Leu Leu Val Ala Thr Ser Leu Trp Arg Gln Gln Gln
245 250 255

Pro Pro Ala Pro Ala Pro Ala Ala Gln Gly Ala Ser Ser Arg Pro Gln
260 265 270

Ala Ser Ala Leu Glu Ile Arg Gly Phe Gln Arg Asp Leu Ser Ser Leu
275 280 285

Arg Arg Leu Ala Gln Ser Phe Arg Pro Ala Met Arg Arg Val Phe Leu
290 295 300

His Glu Ala Thr Ala Arg Leu Met Ala Gly Ala Ser Pro Thr Arg Thr
305 310 315 320

His Gln Leu Leu Asp Arg Ser Leu Arg Arg Arg Ala Gly Pro Gly Gly
325 330 335

Lys Gly Gly Ala Ala Glu Leu Glu Pro Arg Pro Thr Arg Arg Glu His
340 345 350

Ala Glu Ala Leu Leu Ala Ser Cys Tyr Leu Pro Pro Gly Phe Leu
355 360 365

Ser Ala Pro Gly Gln Arg Val Gly Met Leu Ala Glu Ala Arg Thr Leu
370 375 380

Glu Lys Leu Gly Asp Arg Arg Leu Leu His Asp Cys Gln Gln Met Leu
385 390 395 400

Met Arg Leu Gly Gly Thr Thr Val Thr Ser Ser
405 410

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Glu Lys Met Ser Leu Arg Asn Arg Leu Ser Lys Ser Arg Glu Asn Pro
1 5 10 15

Glu Glu Asp Glu Asp Gln Arg Asn Pro Ala Lys Glu Ser Leu Glu Thr
20 25 30

Pro Ser Asn Gly Arg Ile Asp Ile Lys Gln Leu Ile Ala Lys Lys Ile
35 40 45

Lys Leu Thr Ala Glu Asn Gly Arg Ile Asp Ile Lys Gln Leu Ile Ala
50 55 60

Lys Lys Ile Lys Leu Thr Ala Glu Ala Glu Glu Leu Lys Pro Phe Phe
65 70 75 80

Met Lys Glu Val Gly Ser His Phe Asp Asp Phe Val Thr Asn Leu Ile
85 90 95

Glu Lys Ser Ala Ser Leu Asp Asn Lys Ala His Ser Phe Val Arg Glu
100 105 110

Asn Val Pro Arg Val Leu Asn Ser Ala Lys Glu Lys
115 120

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Glu Lys Leu Pro Ile Asn Arg Leu Ala Ala Gly Ser Lys Ala Pro Ala
1 5 10 15

Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr Ala His Asn Ala Ile Glu
 20 25 30

Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys Ile Ile Glu Leu Lys Asp
 35 40 45

Leu Val Val Gly Thr Glu Ala Lys Leu Asn Lys Ser Tyr Ile Arg Phe
 50 55 60

Leu Gln His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu Arg
 65 70 75 80

Thr Ala Val His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala Cys
 85 90 95

Gly Ser Gly Gly Asn Thr Asp Val Leu Met Glu Gly Val Lys Thr Glu
 100 105 110

Val Glu Asp Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg
 115 120 125

Gly Met Leu Asp Arg Ser Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Arg Arg His Cys Pro Leu Lys Asn Pro Thr Phe Leu Asp Tyr Val Arg
 1 5 10 15

Pro Arg Ser Trp Thr Cys Arg Tyr Val Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Ser	Gln	Ile	Gln	Gln	Val	Pro	Val	Leu	Leu	Gln	Pro	His	Phe	Ile	Lys
1					5					10					15
Ala	Asp	Ser	Leu	Leu	Leu	Thr	Ala	Met	Lys	Thr	Asp	Gly	Ala	Thr	Val
			20					25						30	
Lys	Ala	Ala	Gly	Leu	Ser	Pro	Leu	Val	Ser	Gly	Thr	Thr			
				35			40						45		

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Ser	Leu	Leu	Ser	Phe	Met	Gln	Gly	Tyr	Met	Lys	His	Ala	Thr	Lys	Thr
1					5				10						15
Ala	Lys	Asp	Ala	Leu	Ser	Ser	Val	Gln	Glu	Ser	Gln	Val	Ala	Gln	Gln
				20				25						30	
Ala	Arg	Gly	Trp	Val	Thr	Asp	Gly	Phe	Ser	Ser	Leu	Lys			
				35			40						45		

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala	Pro	Ala	Ser	Ala	Gln	Ser	Arg	Gly	Glu	Lys	Arg	Thr	Ala	His	Asn
1						5				10					15
Ala	Ile	Glu	Lys	Arg	Tyr	Arg	Ser	Ser	Ile	Asn	Asp	Lys	Ile	Ile	Glu
				20				25					30		
Leu	Lys	Asp	Leu	Val	Val	Gly	Thr	Glu	Ala	Lys	Leu	Asn	Lys	Ser	
				35			40						45		

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Asp	Tyr	Trp	Ser	Thr	Val	Lys	Asp	Lys	Phe	Ser	Glu	Phe	Trp	Asp	Leu
1					5				10					15	
Asp	Pro	Glu	Val	Arg	Pro	Thr	Ser	Ala	Val	Ala	Ala				
			20				25								

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Glu	Ile	Tyr	Val	Ala	Ala	Ala	Leu	Arg	Val	Lys	Thr	Ser	Leu	Pro	Arg
1					5				10					15	
Ala	Leu	His	Phe	Leu	Thr	Arg	Phe	Phe	Leu	Ser	Ser	Ala	Arg	Gln	Ala
			20			25							30		

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Glu	Lys	Ile	Pro	Thr
1		5		

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Glu Lys Leu Pro Ile
1 5

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Glu Asn Gly Arg Cys Ile Gln Ala Asn Tyr Ser Leu Met Glu Asn Gly
1 5 10 15
Lys Ile Lys Val Leu Asn Gln Glu Leu Arg Ala Asp Gly
20 25

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln His Ser
1 5 10 15
Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu Arg Thr Ala Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr
1 5 10 15

His Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Lys His Glu Ile Gln Glu Met Phe Asp Gln Leu Arg Ala Lys Glu Lys
1 5 10 15
Glu Leu Arg Thr Trp Glu Glu Glu Leu Thr Arg Ala Ala Leu Gln Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Glu Glu Leu Leu Arg Arg Arg Glu Gln Glu Leu Ala Glu Arg Glu Ile
1 5 10 15
Asp Ile Leu Glu Arg Glu Leu Asn Ile Ile Ile His Gln Leu Cys Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Arg Ile Gln Ile Gln Glu Lys Leu Gln Gln Leu Lys Arg His Ile Gln
1 5 10 15
Asn Ile Asp Ile Gln His Leu Ala Gly Lys Leu Lys Gln His Ile Glu
20 25 30

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Val	Leu	Gln	Gln	Val	Lys	Ile	Lys	Asp	Tyr	Phe	Glu	Lys	Leu	Val	Gly
1				5				10						15	
Phe	Ile	Asp	Asp	Ala	Val	Lys	Lys	Leu	Asn	Glu	Leu	Ser	Phe	Lys	Thr
		20				25						30			
Phe	Ile	Glu													
		35													

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Glu	Leu	Ser	Phe	Lys	Thr	Phe	Ile	Glu	Asp	Val	Asn	Lys	Phe	Leu	Asp
1				5				10				15			
Met	Leu	Ile	Lys	Lys	Leu	Lys	Ser	Phe	Asp	Tyr	His	Gln	Phe	Val	
		20					25				30				

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

His	Gln	Phe	Val	Asp	Glu	Thr	Asn	Asp	Lys	Ile	Arg	Glu	Val	Thr	Gln
1				5				10				15			
Arg	Leu	Asn	Gly	Glu	Ile	Gln	Ala	Leu	Glu	Leu	Pro				
		20					25								

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Ala	Ala	Lys	Asn	Leu	Thr	Asp	Phe	Ala	Glu	Gln	Tyr	Ser	Ile	Gln	Asp
1				5					10						15
Trp	Ala	Lys	Arg	Met	Lys	Ala	Leu	Val	Glu	Gln	Gly	Phe	Thr	Val	
	20						25						30		

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Ser	Ala	Ser	Leu	Ala	His	Met	Lys	Ala	Lys	Phe	Arg	Glu	Thr	Leu	Glu
1				5					10						15
Asp	Thr	Arg	Asp	Arg	Met	Tyr	Asp	Met	Asp	Ile	Gln	Gln	Glu	Leu	Gln
	20						25						30		
Arg	Tyr	Leu													
		35													

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Cys	Leu	Asn	Leu	His	Lys	Phe	Asn	Glu	Phe	Ile	Gln	Asn	Glu	Leu	Gln
1					5				10						15
Glu	Ala	Ser	Gln	Glu	Leu	Gln	Gln	Ile	His	Gln	Tyr	Ile	Met	Ala	Leu
	20						25						30		

Arg Glu Glu
35

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Phe Leu Ile Tyr Ile Thr Glu Leu Leu Lys Lys Leu Gln Ser Thr Thr
1 5 10 15

Val Met Asn Pro Tyr Met Lys Leu Ala Pro Gly Glu Leu Thr Ile Ile
20 25 30

Leu

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Arg Leu Leu Asp His Arg Val Pro Glu Thr Asp Met Thr Phe Arg His
1 5 10 15

Val Gly Ser Lys Leu Ile Val Ala Met Ser Ser Trp Leu Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Leu Asn Phe Ser Lys Leu Glu Ile Gln Ser Gln Val Asp Ser Gln His
1 5 10 15

Val Gly His Ser Val Leu Thr Ala Lys Gly Met Ala Leu Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Asn Gln Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His
1 5 10 15

Val Gly Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile
20 25 30

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Val Val Thr Arg Ile Ala Pro Ser Pro Thr Gly Asp Pro His Val
1 5 10 15

Gly Thr Ala Tyr Ile Ala Leu Phe Asn Tyr Ala Trp Ala
20 25

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Thr Thr Val His Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His
1 5 10 15

Ile Gly His Ala Lys Ser Ile Cys Leu Asn Phe Gly Ile Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Lys	Ile	Lys	Leu	Tyr	Cys	Gly	Val	Asp	Pro	Thr	Ala	Gln	Ser	Leu	His
1			5					10						15	
Leu	Gly	Asn	Leu	Val	Pro	Met	Val	Leu	Leu	His	Phe	Tyr	Val		
	20						25						30		

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Pro	Ile	Ala	Leu	Tyr	Cys	Gly	Phe	Asp	Pro	Thr	Ala	Asp	Ser	Leu	His
1			5					10						15	
Leu	Gly	His	Leu	Val	Pro	Leu	Leu	Cys	Leu	Lys	Arg	Gly	Gln		
	20						25						30		

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Arg	Val	Thr	Leu	Tyr	Cys	Gly	Phe	Asp	Pro	Thr	Ala	Asp	Ser	Leu	His
1			5					10						15	
Ile	Gly	Asn	Leu	Ala	Ala	Ile	Leu	Thr	Leu	Arg	Arg	Phe	Gln		
	20						25						30		

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Arg Ile Gly Ala Tyr Val Gly Ile Asp Pro Thr Ala Pro Ser Leu His
1 5 10 15
Val Gly His Leu Leu Pro Leu Met Pro Leu Phe Trp Met Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Pro Ile Ala Leu Tyr Cys Gly Phe Asp Pro Thr Ala Asp Ser Leu His
1 5 10 15
Leu Gly His Leu Val Pro Leu Leu Cys Leu Lys Arg Phe Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro Leu Lys Val Lys Leu Gly Ala Asp Pro Thr Ala Pro Asp Ile His
1 5 10 15
Ile Gly His His Thr Val Val Leu Asn Lys Leu Arg Gln Phe Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Val Ser Lys Gly Leu Leu Ile Phe Asp Ala Ser Ser Ser Met Gly Pro
1 5 10 15

Gln Met Ser Ala Ser Val His Leu Asp Ser Lys Lys Lys Gln His Leu
20 25 30

Phe Val Lys Glu Val Lys Ile Asp Gly Gln Phe
35 40

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Thr Ile Ile Thr Thr Pro Pro Leu Lys Asp Phe Ser Leu Trp Glu Lys
1 5 10 15

Thr Gly Leu Lys Glu Phe Leu Lys Thr Thr Lys Gln Ser Phe Asp Leu
20 25 30

Ser Val Lys Ala Gln Tyr Lys Lys Asn Lys His
35 40

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Lys Asn Arg Asn Asn Ala Leu Asp Phe Val Thr Lys Ser Tyr Asn Glu
1 5 10 15

Thr Lys Ile Lys Phe Asp Lys Tyr Lys Ala Glu Lys Ser Gln Asp Glu
20 25 30

Leu Pro Arg Thr Phe Gln Ile
35

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr Thr Arg Leu Thr Arg Lys
1 5 10 15

Arg Gly Leu Lys Leu Ala Thr Ala Leu Ser Leu Ser Asn Lys Phe Val
20 25 30

Glu Gly Ser His
35

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Arg Ala Phe Gly Trp Glu Ala Pro Arg Phe Tyr His Met Pro Leu Leu
1 5 10 15

Arg Asn Pro Asp Lys Thr Lys Ile Ser Lys Arg Lys Ser His Thr Ser
20 25 30

Leu Asp Trp Tyr Lys Ala Glu Gly Phe Leu
35 40

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asp Asn Ile Thr Ile Pro Val His Pro Arg Gln Tyr Glu Phe Ser Arg
1 5 10 15
Leu Asn Leu Glu Tyr Thr Val Met Ser Lys Arg Lys Leu Asn Leu Leu
20 25 30
Val Thr Asp Lys His Val Glu Gly Trp Asp
35 40

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Lys Asn Lys Gly Leu Pro Phe Gly Ile Thr Val Pro Leu Leu Thr Thr
1 5 10 15
Ala Thr Gly Glu Lys Phe Gly Lys Ser Ala Gly Asn Ala Val Phe Ile
20 25 30
Asp Pro Ser Ile Asn Thr Ala Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg Leu His Gln Asn Gln Val Phe Gly Leu Thr Val Pro Leu Ile Thr
1 5 10 15
Lys Ala Asp Gly Thr Lys Phe Gly Lys Thr Glu Gly Gly Ala Val Trp
20 25 30
Leu Asp Pro Lys Lys Thr Ser Pro Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Lys Thr Lys Gly Glu Ala Arg Ala Phe Gly Leu Thr Ile Pro Leu Val
1 5 10 15

Thr Lys Ala Asp Gly Thr Lys Phe Gly Lys Thr Glu Ser Gly Thr Ile
20 25 30

Trp Leu Asp Lys Glu Lys Thr Ser Pro Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Lys Thr Ala Leu Asp Glu Cys Val Gly Phe Thr Val Pro Leu Leu Thr
1 5 10 15

Asp Ser Ser Gly Ala Lys Phe Gly Lys Ser Ala Gly Asn Ala Ile Trp
20 25 30

Leu Asp Pro Tyr Gln Thr Ser Val Phe
35 40

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Arg Leu His Gln Asn Gln Val Phe Gly Leu Thr Val Pro Leu Ile Thr
1 5 10 15

Lys Ala Asp Gly Thr Lys Phe Gly Lys Thr Glu Gly Gly Ala Val Trp
20 25 30

Leu Asp Pro Lys Lys Thr Ser Pro Tyr
35 40

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Ala Gly Lys Lys Pro Gln Val Ala Ile Thr Leu Pro Leu Leu Val
1 5 10 15

Gly Leu Asp Gly Glu Lys Lys Met Ser Lys Ser Leu Gly Asn Tyr Ile
20 25 30

Gly Val Thr Glu Ala Pro Ser Asp Met Phe
35 40

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Arg Val Ser Thr Ala Phe Val Tyr Thr Lys Asn Pro Asn Gly Tyr Ser
1 5 10 15

Phe Ser Ile Pro Val Lys Val Leu Ala Asp Lys Phe Ile Thr Pro Gly
20 25 30

Leu Lys Leu
35

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn
1 5 10 15

Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly
20 25

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

His Ile Gly His
1

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

His Lys Asn Thr Ser Thr Leu Ser Cys Asp Gly Ser Leu Arg His Lys
1 5 10 15

Phe

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Arg Lys Leu Lys His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg His Ile Gln Asn Ile Asp Ile Gln His Leu Ala Gly Lys Leu Lys
1 5 10 15

Gln His

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Lys Lys Gly Phe Tyr Lys Lys Gln Cys Arg Pro Ser Lys Gly Arg
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg
1 5 10 15

Glu Arg

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Lys Lys Thr Asn Leu Phe Ser Ala Leu Ile Lys Lys Lys Lys Thr
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Arg Lys Thr Leu Leu Asn Ser Leu Glu Glu Ala Lys Lys Lys Lys Glu
1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Arg Glu Leu Asp Glu Ser Leu Gln Val Ala Glu Arg Leu Thr Arg
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Arg Arg Ser Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu Arg
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Arg Arg Tyr Gly Asp Glu Glu Leu His Leu Cys Val Ser Arg Lys His
1 5 10 15

Phe

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Gln Asn Arg Glu Arg Arg
1 5 10 15
Arg

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg Lys
1 5 10 15
Phe

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Lys Arg Pro Pro Ile Ser Asp Ser Glu Glu Leu Ser Ala Lys Lys Arg
1 5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Lys Lys Gly Lys Lys Pro Lys Thr Glu Lys Glu Asp Lys Val Lys His
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Arg His Ile Gln Asn Ile Asp Ile Gln His Leu Ala Gly Lys Leu Lys
1 5 10 15

Gln His

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Lys Lys Ile Thr Glu Val Ala Leu Met Gly His Leu Ser Cys Asp Thr
1 5 10 15

Lys Glu Glu Arg Lys
20

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Lys His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

His Arg Asn Ile Gln Glu Tyr Leu Ser Ile Leu Thr Asp Pro Asp Gly
1 5 10 15

Lys Gly Lys Glu Lys
20

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Lys Glu Val Tyr Gly Phe Asn Pro Glu Gly Lys Ala Leu Leu Lys Lys
1 5 10 15

Thr Lys

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Lys Val Leu Val Asp His Phe Gly Tyr Thr Lys Asp Asp Lys His Glu
1 5 10 15

Asp Met

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Arg Gln Val Ser His Ala Lys Glu Lys Leu Thr Ala Leu Thr Lys Lys
1 5 10 15

Tyr Arg

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Lys Tyr Gln Ile Arg Ile Gln Ile Gln Glu Lys Leu Gln Gln Leu Lys
1 5 10 15

Arg His

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Lys Tyr Gln Ile Arg Ile Gln Ile Gln Glu Lys Leu Gln Gln Leu Lys
1 5 10 15

Arg His

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala Glu Phe Thr Gly Arg
1 5 10 15

His Asp Ala His
20

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys Gln Ser Phe Asp Leu Ser Val Lys Ala Gln Tyr Lys Lys Asn Lys
1 5 10 15
His Arg

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Lys Leu Glu Gly Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Lys Leu Asp Val Thr Thr Ser Ile Gly Arg Arg Gln His Leu Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Lys Lys Leu Asp Phe Arg Glu Ile Gln Ile Tyr Lys Lys Leu Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Lys Ser Pro Ala Thr Asp Leu His Leu Arg Tyr Gln Lys Asp Lys Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Lys Tyr His Trp Glu His Thr Gly Leu Thr Leu Arg Glu Val Ser Ser
1 5 10 15

Lys Leu Arg Arg
20

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Lys Asp Asn Val Phe Asp Gly Leu Val Arg Val Thr Gln Lys Phe His
1 5 10 15

Met Lys Val Lys His
20

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Ser Ile Asn Leu Pro Phe Phe Glu Thr Leu Gln Glu Tyr Phe Glu Arg
1 5 10 15

Asn Arg Gln Thr Ile Ile Val Val Val Glu Asn Val Gln Arg Asn Leu
20 25 30

Lys His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg Ala Ala Leu
35 40 45

Gly Lys Leu Pro Gln Gln Ala Asn Asp Tyr Leu Asn Ser Phe Asn Trp
50 55 60

Glu Arg Gln Val Ser His Ala Lys Glu Lys Leu Thr Ala Leu Thr Lys
65 70 75 80

Lys Tyr Arg Ile Thr Glu Asn Asp Ile Gln Ile Ala Leu Asp Asp Ala
85 90 95

Lys Ile Asn Phe Asn Glu Lys Leu Ser Gln Leu Gln Thr Tyr Met Ile
100 105 110

Gln Phe Asp Gln Tyr Ile Lys Asp Ser Tyr Asp Leu His Asp Leu Lys
115 120 125

Ile Ala Ile Ala Asn Ile Ile Asp Glu Ile Ile Glu Lys Leu Lys Ser
130 135 140

Leu Asp Glu His Tyr His Ile Arg Val Asn Leu Val Lys Thr Ile His
145 150 155 160

Asp Leu His Leu Phe Ile Glu Asn Ile Asp Phe Asn Lys Ser Gly Ser
165 170 175

Ser Thr Ala Ser
180

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Pro Gln Gln Val Asn Asp Tyr Leu Ser Thr Phe Ser Trp Glu Arg Gln
1 5 10 15

Val Leu Ser Ala Lys Lys His Ser Asp Phe Met Glu Asp Tyr Arg
20 25 30

Ile Thr Glu Asn Asp Val Arg Ile Ala Leu Asp Asn Ala Lys Ile Asn
35 40 45

Leu Asn Glu Lys Leu Thr Gln Leu Gln Thr Tyr Val Ile Gln Phe Asp
50 55 60

Gln Tyr Ile Lys Asp Asn Tyr Asp Leu His Asp Phe Lys Thr Ala Ile
65 70 75 80

Ala Arg Ile Ile Asp Glu Ile Ile Ala Thr Leu Lys Ile Leu
85 90

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Lys Tyr Arg Val Ala Leu Ser Arg Leu Pro Gln Gln Ile His Asp Tyr
1 5 10 15

Leu Asn Ala Ser Asp Trp Glu Arg Gln Val Ala Gly Ala Lys Glu Lys
20 25 30

Leu Thr Ser Phe Met Glu Asn Tyr Arg Ile Thr Asp Asn Asp Val Leu
35 40 45

Ile Ala Leu Asp Ser Ala Lys Ile Asn Leu Asn Glu Lys Leu Ser Gln
50 55 60

Leu Glu Thr Tyr Ala Ile Gln Phe Asp Gln Tyr Ile Arg Asp Asn Tyr
65 70 75 80

Asp Ala Gln Asp Leu
85

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Leu Asn Asp Phe Gln Val Pro Asp Leu His Ile Pro Glu Phe Gln Leu
1 5 10 15

Pro His Ile Ser His Thr Ile Glu Val Pro Thr Phe Gly Lys Leu Tyr
20 25 30

Ser Ile Leu Lys Ile Gln Ser Pro Leu Phe Thr Leu Asp Ala Asn Ala
35 40 45

Asp Ile Gly Asn Gly Thr Thr Ser Ala Asn Glu Ala Gly Ile Ala Ala
50 55 60

Ser Ile Thr Ala Lys Gly Glu Ser Lys Leu Glu Val Leu Asn Phe Asp
65 70 75 80

Phe Gln Ala Asn Ala Gln Leu Ser Asn Pro Lys Ile Asn Pro Leu Ala
85 90 95

Leu Lys Glu Ser Val Lys Phe Ser Ser Lys Tyr Leu Arg Thr Glu His
100 105 110

Gly Ser Glu Met Leu Phe Phe Gly Asn Ala Ile Glu Gly Lys Ser Asn
115 120 125

Thr Val Ala Ser Leu His Thr Glu Lys Asn Thr Leu Glu Leu Ser Asn
130 135 140

Gly Val Ile Val Lys Ile Asn Asn Gln Leu Thr Leu Asp Ser Asn Thr
145 150 155 160

Lys Tyr Phe His Lys Leu Asn Ile Pro Lys Leu Asp Phe Ser Ser Gln
165 170 175

Ala Asp Leu Arg Asn Glu Ile Lys Thr Leu Leu Lys Ala Gly His Ile
180 185 190

Ala Trp Thr Ser Ser Gly Lys Gly Ser Trp Lys Trp Ala Cys Pro Arg
195 200 205

Phe Ser Asp Glu Gly Thr His Glu Ser Gln Ile Ser Phe Thr Ile Glu
210 215 220

Gly Pro Leu Thr Ser Phe Gly Leu Ser Asn Lys Ile Asn Ser Lys His
225 230 235 240

Leu Arg Val Asn Gln Asn Leu Val Tyr Glu Ser Gly Ser Leu Asn Phe
245 250 255

Ser Lys Leu Glu Ile Gln Ser Gln Val Asp Ser Gln His Val Gly His
260 265 270

Ser Val Leu Thr Ala Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala
275 280 285

Glu Phe Thr Gly Arg His Asp Ala His Leu Asn Gly Lys Val Ile Gly
290 295 300

Thr Leu Lys Asn Ser Leu Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr
305 310 315 320

Ala Ser Thr Asn Asn Glu Gly Asn Leu Lys Val Arg Phe Pro Leu Arg
325 330 335

Leu Thr Gly Lys Ile Asp Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser
340 345 350

Pro Ser Ala Gln Gln Ala Ser Trp Gln Val Ser Ala Arg Phe Asn Gln
355 360 365

Tyr Lys Tyr Asn Gln Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met
370 375 380

Glu Ala His Val Gly Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn
385 390 395 400

Ile Pro Leu Thr Ile Pro Glu Met Arg Leu Pro Tyr Thr Ile Ile Thr
405 410 415

Thr Pro Pro Leu Lys Asp Phe Ser Leu Trp Glu Lys Thr Gly Leu Lys
420 425 430

Glu Phe Leu Lys Thr Thr Lys Gln Ser Phe Asp Leu Ser Val Lys Ala
435 440 445

Gln Tyr Lys Lys Asn Lys His Arg His Ser Ile Thr Asn Pro Leu Ala
450 455 460

Val Leu Cys Glu Phe Ile Ser Gln Ser Ile Lys Ser Phe Asp Arg His
465 470 475 480

Phe Glu Lys Asn Arg Asn Asn Ala Leu Asp Phe Val Thr Lys Ser Tyr
485 490 495

Asn Glu Thr Lys Ile Lys Phe Asp Lys Tyr Lys Ala Glu Lys Ser His
500 505 510

Asp Glu Leu Pro Arg Thr Phe Gln Ile Pro Gly Tyr Thr Val Pro Val
515 520 525

Val Asn Val Glu Val Ser Pro Phe Thr Ile Glu Met Ser Ala Phe Gly
530 535 540

Tyr Val Phe Pro Lys Ala Val Ser Met Pro Ser Phe Ser Ile Leu Gly
545 550 555 560

Ser Asp Val Arg Val Pro Ser Tyr Thr Leu Ile Leu Pro Ser Leu Glu
565 570 575

Leu Pro Val Leu His Val Pro Arg Asn Leu Lys Leu Ser Leu Pro His
580 585 590

Phe Lys Glu Leu Cys Thr Ile Ser His Ile Phe Ile Pro Ala Met Gly
595 600 605

Asn Ile Thr Tyr Asp Phe Ser Phe Lys Ser Ser Val Ile Thr Leu Asn
610 615 620

Thr Asn Ala Glu Leu Phe Asn Gln Ser Asp Ile Val Ala His Leu Leu
625 630 635 640

Ser Ser Ser Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu Gly
645 650 655

Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys Leu Ala Thr Ala Leu
660 665 670

Ser Leu Ser Asn Lys Phe Val Glu Gly Ser His Asn Ser Thr Val Ser
675 680 685

Leu Thr Thr Lys Asn Met Glu Val Ser Val Ala Lys Thr Thr Lys Ala
690 695 700

Glu Ile Pro Ile Leu Arg Met Asn Phe Lys Gln Glu Leu Asn Gly Asn
705 710 715 720

Thr Lys Ser Lys Pro Thr Val Ser Ser Met Glu Phe Lys Tyr Asp
725 730 735

Phe Asn Ser Ser Met Leu Tyr Ser Thr Ala Lys Gly Ala Val Asp His
740 745 750

Lys Leu Ser Leu Glu Ser Leu Thr Ser Tyr Phe Ser Ile Glu Ser Ser
755 760 765

Thr Lys Gly Asp Val Lys Gly Ser Val Leu Ser Arg Glu Tyr Ser Gly
770 775 780

Thr Ile Ala Ser Glu Ala Asn Thr Tyr Leu Asn Ser Lys Ser Thr Arg
785 790 795 800

Ser Ser Val Lys Leu Gln Gly Thr Ser Lys Ile Asp Asp Ile Trp Asn
805 810 815

Leu Glu Val Lys Glu Asn Phe Ala Gly Glu Ala Thr Leu Gln Arg Ile
820 825 830

Tyr Ser Leu Trp Glu His Ser Thr
835 840

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Glu Phe Gln Leu Pro Arg Leu Ser His Thr Ile Glu Ile Pro Ala Phe
1 5 10 15

Gly Arg Leu His Gly Ile Leu Lys Ile Gln Ser Pro Leu Phe Ile Leu
20 25 30

Asp Ala Asn Ala Asn Ile Gln Asn Val Thr Thr Leu Glu Asn Lys Ala
35 40 45

Glu Ile Val Ala Ser Ile Ala Ala Thr Gly Glu Ser Glu Ile Glu Ala
50 55 60

Leu Asn Phe Asp Phe Gln Ala Gln Ala Gln Phe Leu Glu Leu Asn Pro
65 70 75 80

Asn Pro Leu Ile Leu Lys Glu Ser Met Asn Phe Ser Ser Lys His Ala
85 90 95

Arg Met Glu His Glu Gly Glu Ile Leu Phe Ser Gly Lys Phe Ile Glu
100 105 110

Gly Lys Leu Asp Thr Val Ala Ser Leu Gln Thr Glu Lys Asn Met Val
115 120 125

Glu Phe Asn Asn Gly Met Ile Val Lys Ile Asn Asn Pro Ile Ile Leu
130 135 140

Asp Ser His Thr Lys Tyr Phe His Lys Leu Ser Ile Pro Arg Leu Asp
145 150 155 160

Phe Ser Ser Lys Ala Ser Phe Asn Asn Glu Ile Lys Met Leu Leu Glu
165 170 175

Ala Gly His Val Ala Trp Thr Ser Ser Gly Thr Gly Ser Trp Asn Trp
180 185 190

Ala Cys Pro Asn Phe Ser Asp Glu Gly Thr His Ser Ser Lys Ile Ser
195 200 205

Phe Thr Val Glu Gly Pro Ile Ala Phe Phe Gly Leu Ser Asn Asn Ile
210 215 220

Asn Gly Lys His Leu Arg Val Ile Gln Lys Leu Ala Tyr Glu Ser Gly
225 230 235 240

Phe Leu Asn Tyr Ser Met Leu Glu Val Glu Ser Lys Val Glu Ser Gln
245 250 255

His Val Gly Ser Ser Ile Leu Thr Gly Lys Gly Thr Val Leu Leu Arg
260 265 270

Glu Ala Lys Ala Glu Met Thr Gly Glu His Asn Ala Asp Leu Asn Gly
275 280 285

Lys Val Ile Gly Thr Leu Lys Asn Ser Leu Ser Phe Ser Ala Gln Pro
290 295 300

Phe Met Ile Thr Ala Ser Thr Asn Asn Asp Gly Asn Leu Lys Val Ser
305 310 315 320

Phe Pro Leu Lys Leu Thr Gly Lys Ile Asp Phe Leu Asn Asn Tyr Ala
325 330 335

Leu Phe Leu Ser Pro His Ala Gln Gln Ala Ser Trp Gln Val Ser Ala
340 345 350

Arg Phe Asn Tyr Lys Tyr Asn Gln Asn Phe Ser Ala Ile Asn Asn Glu
355 360 365

His Asn Ile Glu Ala His Val Gly Met Asn Gly Asp Ala Asn Leu Asp
370 375 380

Phe Leu Thr Ile Pro Leu Thr Ile Pro Glu Val Lys Leu Pro Tyr Ile
385 390 395 400

Gly Leu Thr Thr Pro Leu Leu Lys Asp Phe Ser Ile Trp Glu Glu Thr
405 410 415

Gly Leu Lys Lys Gln Ser Phe Asp Leu Ser Val Lys Ala Gln Tyr Lys
420 425 430

Lys Asn Arg Asp Arg His Ser Ile Ala Ile Pro Leu Asn Gly Phe Tyr
435 440 445

Glu Phe Ile Leu Asn Asn Val Asp Ser Gly Ile Gly Lys Ile Gly Lys
450 455 460

Val Arg Asp Ser Ala Leu Asp Tyr Leu Ile Ser Ser Tyr Asn Glu Ala
465 470 475 480

Lys Asn Lys Phe Glu Asn Ser Leu Ile Gln Pro Ser Arg Thr Phe Gln
485 490 495

Lys Arg Gly Tyr Thr Ile Pro Phe Val Asn Ile Glu Val Thr Pro Phe
500 505 510

Thr Val Glu Thr Leu Ala Ser Ser His Val Ile Pro Lys Ala Ile Asn
515 520 525

Thr Pro Ser Val His Ile Leu Gly Pro Asn Val Ile Val Pro Ser Tyr
530 535 540

Arg Leu Val Leu Pro Ser Leu Glu Leu Pro Val Leu Arg Val Pro Arg
545 550 555 560

Asn Leu Leu Lys Phe Ser Leu Pro Asp Phe Lys Glu Leu Arg Thr Ile
565 570 575

Asp Asn Ile Tyr Ile Pro Ala Leu Gly Asn Phe Thr Tyr Asp Phe Ser
580 585 590

Phe Lys Ser Ser Val Ile Thr Leu Asn Thr Asn Val Gly Leu Tyr Asn
595 600 605

Arg Ser Asp Ile Val Ala His Phe Leu Ser Ser Ser Phe Val Thr
610 615 620

Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr Ser Arg Leu Thr Arg Lys
625 630 635 640

Arg Gly Leu Lys Leu Ala Thr Ala Asp Ser Leu Thr Asn Lys Phe Val
645 650 655

Lys Gly Asn His Asp Ser Thr Phe Ser Leu Thr Lys Lys Asn Met Glu
660 665 670

Ala Ser Val Lys Thr Thr Ala Asn Leu His Ala Pro Ile Leu Thr Met
675 680 685

Asn Phe Lys Gln Glu Leu Asn Gly Asn Ala Lys Ser Lys Pro Ile Val
690 695 700

Ser Ser Ser Ile Glu Leu Asn Tyr Asp Phe Asn Ser Ser Lys Leu Tyr
705 710 715 720

Ser Thr Ala Lys Gly Gly Val Asp His Lys Phe Ser Leu Glu Ser Leu
725 730 735

Thr Ser Tyr Phe Ser Ile Glu Ser Ser Thr Lys Gly Asn Ile Lys Gly
740 745 750

Ser Val Leu Ser Gln Glu Tyr Ser Gly Ser Val Ala Ser Glu Ala Asn
755 760 765

Thr Tyr Leu Asn Ser
770

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu Phe Gln Leu Pro His Leu Ser His Thr Ile Glu Ile Pro Ala Phe
1 5 10 15

Gly Lys Leu His Ser Ile Leu Lys Ile Gln Ser Pro Leu Phe Ile Leu
20 25 30

Asp Ala Asn Ala Asn Ile Gln Asn Val Thr Thr Ser Gly Asn Lys Ala
35 40 45

Glu Ile Val Ala Ser Val Thr Ala Lys Gly Glu Ser Gln Phe Glu Ala
50 55 60

Leu Asn Phe Asp Phe Gln Ala Gln Ala Gln Phe Leu Glu Leu Asn Pro
65 70 75 80

His Pro Pro Val Leu Lys Glu Ser Met Asn Phe Ser Ser Lys His Val
85 90 95

Arg Met Glu His Glu Gly Glu Ile Val Phe Asp Gly Lys Ala Ile Glu
100 105 110

Gly Lys Ser Asp Thr Val Ala Ser Leu His Thr Glu Lys Asn Glu Val
115 120 125

Glu Phe Asn Asn Gly Met Thr Val Lys Val Asn Asn Gln Leu Thr Leu
130 135 140

Asp Ser His Thr Lys Tyr Phe His Lys Leu Ser Val Pro Arg Leu Asp
145 150 155 160

Phe Ser Ser Lys Ala Ser Leu Asn Asn Glu Ile Lys Thr Leu Leu Glu
165 170 175

Ala Gly His Val Ala Leu Thr Ser Ser Gly Thr Gly Ser Trp Asn Trp
180 185 190

Ala Cys Pro Asn Phe Ser Asp Glu Gly Ile His Ser Ser Gln Ile Ser
195 200 205

Phe Thr Val Asp Gly Pro Ile Ala Phe Val Gly Leu Ser Asn Asn Ile
210 215 220

Asn Gly Lys His Leu Arg Val Ile Gln Lys Leu Thr Tyr Glu Ser Gly
225 230 235 240

Phe	Leu	Asn	Tyr	Ser	Lys	Phe	Glu	Val	Glu	Ser	Lys	Val	Glu	Ser	Gln
245						250						255			
His	Val	Gly	Ser	Ser	Ile	Leu	Thr	Ala	Asn	Gly	Arg	Ala	Leu	Leu	Lys
260						265						270			
Asp	Ala	Lys	Ala	Glu	Met	Thr	Gly	Glu	His	Asn	Ala	Asn	Leu	Asn	Gly
275						280						285			
Lys	Val	Ile	Gly	Thr	Leu	Lys	Asn	Ser	Leu	Phe	Phe	Ser	Ala	Gln	Pro
290						295						300			
Phe	Glu	Ile	Thr	Ala	Ser	Thr	Asn	Asn	Glu	Gly	Asn	Leu	Lys	Val	Gly
305						310						315			320
Phe	Pro	Leu	Lys	Leu	Thr	Gly	Lys	Ile	Asp	Phe	Leu	Asn	Asn	Tyr	Ala
325						330								335	
Leu	Phe	Leu	Ser	Pro	Arg	Ala	Gln	Gln	Ala	Ser	Trp	Gln	Ala	Ser	Thr
340						345								350	
Arg	Phe	Asn	Gln	Tyr	Lys	Tyr	Asn	Gln	Asn	Phe	Ser	Ala	Ile	Asn	Asn
355						360								365	
Glu	His	Asn	Ile	Glu	Ala	Ser	Ile	Gly	Met	Asn	Gly	Asp	Ala	Asn	Leu
370						375						380			
Asp	Phe	Leu	Asn	Ile	Pro	Leu	Thr	Ile	Pro	Glu	Ile	Asn	Leu	Pro	Tyr
385						390						395			400
Thr	Glu	Phe	Lys	Thr	Pro	Leu	Leu	Lys	Asp	Phe	Ser	Ile	Trp	Glu	Glu
405						410								415	
Thr	Gly	Leu	Lys	Glu	Phe	Leu	Lys	Thr	Thr	Lys	Gln	Ser	Phe	Asp	Leu
420						425								430	
Ser	Val	Lys	Ala	Gln	Tyr	Lys	Asn	Ser	Asp	Lys	His	Ser	Ile	Val	
435						440								445	
Val	Pro	Leu	Gly	Met	Phe	Tyr	Glu	Phe	Ile	Leu	Asn	Asn	Val	Asn	Ser
450						455								460	
Trp	Asp	Arg	Lys	Phe	Glu	Lys	Val	Arg	Asn	Asn	Ala	Leu	His	Phe	Leu
465						470								475	
Thr	Thr	Ser	Tyr	Asn	Glu	Ala	Lys	Ile	Lys	Val	Asp	Lys	Tyr	Lys	Thr
485						490								495	
Glu	Asn	Ser	Leu	Asn	Gln	Pro	Ser	Gly	Thr	Phe	Gln	Asn	His	Gly	Tyr
500						505								510	
Thr	Ile	Pro	Val	Val	Asn	Ile	Glu	Val	Ser	Pro	Phe	Ala	Val	Glu	Thr
515						520								525	

Leu Ala Ser Arg His Val Ile Pro Thr Ala Ile Ser Thr Pro Ser Val
530 535 540

Thr Ile Pro Gly Pro Asn Ile Met Val Pro Ser Tyr Lys Leu Val Leu
545 550 555 560

Pro Pro Leu Glu Leu Pro Val Phe His Gly Pro Gly Asn Leu Phe Lys
565 570 575

Phe Phe Leu Pro Asp Phe Lys Gly Phe Asn Thr Ile Asp Asn Ile Tyr
580 585 590

Ile Pro Ala Met Gly Asn Phe Thr Tyr Asp Phe Ser Phe Lys Ser Ser
595 600 605

Val Ile Thr Leu Asn Thr Asn Ala Gly Leu Tyr Asn Gln Ser Asp Ile
610 615 620

Val Ala His Phe Leu Ser Ser Ser Phe Val Thr Asp Ala Leu Gln
625 630 635 640

Tyr Lys Leu Glu Gly Thr Ser Arg Leu Met Arg Lys Arg Gly Leu Lys
645 650 655

Leu Ala Thr Ala Val Ser Leu Thr Asn Lys Phe Val Lys Gly Ser His
660 665 670

Asp Ser Thr Ile Ser Leu Thr Lys Lys Asn Met Glu Ala Ser Val Arg
675 680 685

Thr Thr Ala Asn Leu His Ala Pro Ile Phe Ser Met Asn Phe Lys Gln
690 695 700

Glu Leu Asn Gly Asn Thr Lys Ser Lys Pro Thr Val Ser Ser Ser Ile
705 710 715 720

Glu Leu Asn Tyr Asp Phe Asn Ser Ser Lys Leu His Ser Thr Ala Thr
725 730 735

Gly Gly Ile Asp His Lys Phe Ser Leu Glu Ser Leu Thr Ser Tyr Phe
740 745 750

Ser Ile Glu Ser Phe Thr Lys Gly Asn Ile Lys Ser Ser Phe Leu Ser
755 760 765

Gln Glu Tyr Ser Gly Ser Val Ala Asn Glu Ala Asn Val Tyr Leu Asn
770 775 780

Ser
785

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Glu Tyr Ser Gly Thr Ile Ala Ser Glu Ala Asn Thr Tyr Leu Asn Ser
1 5 10 15

Lys Ser Thr Arg Ser Ser Val Lys Leu Gln Gly Thr Ser Lys Ile Asp
20 25 30

Asp Ile Trp Asn Leu Glu Val Lys Glu Asn Phe Ala Gly Glu Ala Thr
35 40 45

Leu Gln Arg Ile Tyr Ser Leu Trp Glu His Ser Thr Lys Asn His Leu
50 55 60

Gln Leu Glu Gly Leu Phe Phe Thr Asn Gly Glu His Thr Ser Lys Ala
65 70 75 80

Thr Leu Glu Leu Ser Pro Trp Gln Met Ser Ala Leu Val Gln Val His
85 90 95

Ala Ser Gln Pro Ser Ser Phe His Asp Phe Pro Asp Leu Gly Gln Glu
100 105 110

Val Ala Leu Asn Ala Asn Thr Lys Asn Gln Lys Ile Arg Trp Lys Asn
115 120 125

Glu Val Arg Ile His Ser Gly Ser Phe Gln Ser Gln Val Glu Leu Ser
130 135 140

Asn Asp Gln Glu Lys Ala His Leu Asp Ile Ala Gly Ser Leu Glu Gly
145 150 155 160

His Leu Arg Phe Leu Lys Asn Ile Ile Leu Pro Val Tyr Asp Lys Ser
165 170 175

Leu Trp Asp Phe Leu Lys Leu Asp Val Thr Thr Ser Ile Gly Arg Arg
180 185 190

Gln His Leu Arg Val Ser Thr Ala Phe Val Tyr Thr Lys Asn Pro Asn
195 200 205

Gly Tyr Ser Phe Ser Ile Pro Val Lys Val Leu Ala Asp Lys Phe Ile
210 215 220

Thr Pro Gly Leu Lys Leu Asn Asp Leu Asn Ser Val Leu Val Met Pro
225 230 235 240

Thr Phe His Val Pro Phe Thr Asp Leu Gln Val Pro Ser Cys Lys Leu
245 250 255

Asp Phe Arg Glu Ile Gln Ile Tyr Lys Lys Leu Arg Thr Ser Ser Phe
260 265 270

Ala Leu Asn Leu Pro Thr Leu Pro Glu Val Lys Phe Pro Glu Val Asp
275 280 285

Val Leu Thr Lys Tyr Ser Gln Pro Glu Asp Ser Leu Ile Pro Phe Phe
290 295 300

Glu Ile Thr Val Pro Glu Ser Gln Leu Thr Val Ser Gln Phe Thr Leu
305 310 315 320

Pro Lys Ser Val Ser Asp Gly Ile Ala Ala Leu Asp Leu Asn Ala Val
325 330 335

Ala Asn Lys Ile Ala Asp Phe Glu Leu Pro Thr Ile Ile Val Pro Glu
340 345 350

Gln Thr Ile Glu Ile Pro Ser Ile Lys Phe Ser Val Pro Ala Gly Ile
355 360 365

Val Ile Pro Ser Phe Gln Ala Leu Thr Ala Arg Phe Glu Val Asp Ser
370 375 380

Pro Val Tyr Asn Ala Thr Trp Ser Ala Ser Leu Lys Asn Lys Ala Asp
385 390 395 400

Tyr Val Glu Thr Val Leu Asp Ser Thr Cys Ser Ser Thr Val Gln Phe
405 410 415

Leu Glu Tyr Glu Leu Asn Val Leu Gly Thr His Lys Ile Glu Asp Gly
420 425 430

Thr Leu Ala Ser Lys Thr Lys Gly Thr Leu Ala His Arg Asp Phe Ser
435 440 445

Ala Glu Tyr Glu Glu Asp Gly Lys Phe Glu Gly Leu Gln Glu Trp Glu
450 455 460

Gly Lys Ala His Leu Asn Ile Lys Ser Pro Ala Phe Thr Asp Leu His
465 470 475 480

Leu Arg Tyr Gln Lys Asp Lys Lys Gly Ile Ser Thr Ser Ala Ala Ser
485 490 495

Pro Ala Val Gly Thr Val Gly Met Asp Met Asp Glu Asp Asp Asp Phe
500 505 510

Ser Lys Trp Asn Phe Tyr Tyr Ser Pro Gln Ser Ser Pro Asp Lys Lys
515 520 525

Leu Thr Ile Phe Lys Thr Glu Leu Arg Val Arg Glu Ser Asp Glu Glu
530 535 540

Thr Gln Ile Lys Val Asn Trp Glu Glu Glu Ala Ala Ser Gly Leu Leu
545 550 555 560

Thr Ser Leu Lys Asp Asn Val Pro Lys Ala Thr Gly Val Leu Tyr Asp
565 570 575

Tyr Val Asn Lys Tyr His Trp Glu His Thr Gly Leu Thr Leu Arg Glu
580 585 590

Val Ser Ser Lys Leu Arg Arg Asn Leu Gln Asn Asn Ala Glu Trp Val
595 600 605

Tyr Gln Gly Ala Ile Arg Gln Ile Asp Asp Ile Asp Val Arg Phe Gln
610 615 620

Lys Ala Ala Ser Gly Thr Thr Gly Thr Tyr Gln Glu Trp Lys Asp Lys
625 630 635 640

Ala Gln Asn Leu Tyr Gln Glu Leu Leu Thr Gln Glu Gly Gln Ala Ser
645 650 655

Phe Gln Gly Leu Lys Asp Asn Val Phe Asp Gly Leu Val Arg Val Thr
660 665 670

Gln Lys Phe His Met Lys Val Lys His Leu Ile Asp Ser Leu Ile Asp
675 680 685

Phe Leu Asn Phe Pro Arg Phe Gln Phe Pro Gly Lys Pro Gly Ile Tyr
690 695 700

Thr Arg Glu Glu Leu Cys Thr Met Phe Ile Arg Glu Val Gly Thr Val
705 710 715 720

Leu Ser Gln Val Tyr Ser Lys Val His Asn Gly Ser Glu Ile Leu Phe
725 730 735

Ser Tyr Phe Gln Asp Leu Val Ile Thr Leu Pro Phe Glu Leu Arg Lys
740 745 750

His Lys Leu Ile Asp Val Ile Ser Met Tyr Arg Glu Leu Leu Lys Asp
755 760 765

Leu Ser Lys Glu Ala Gln Glu Val Phe Lys Ala Ile Gln Ser Leu Lys
770 775 780

Thr Thr Glu Val Leu Arg Asn Leu Gln Asp Leu Leu Gln Phe Ile Phe
785 790 795 800

Gln Leu Ile Glu Asp Asn Ile Lys Gln Leu Lys Glu Met Lys Phe Thr
805 810 815

Tyr Leu Ile Asn Tyr Ile Gln Asp Glu Ile Asn Thr Ile Phe Asn Asp
 820 825 830
 Tyr Ile Pro Tyr Val Phe Lys Leu Leu Lys Glu Asn Leu Cys Leu Asn
 835 840 845
 Leu His Lys Phe Asn Glu Phe Ile Gln Asn Glu Leu Gln Glu Ala Ser
 850 855 860
 Gln Glu Leu Gln Gln Ile His Gln Tyr Ile Met Ala Leu Arg Glu Glu
 865 870 875 880
 Tyr Phe Asp Pro Ser Ile Val Gly Trp Thr Val Lys Tyr Tyr Glu Leu
 885 890 895
 Glu Glu Lys Ile Val Ser Leu Ile Lys Asn Leu Leu Val Ala Leu Lys
 900 905 910
 Asp Phe His Ser Glu Tyr Ile Val Ser Ala Ser Asn Phe Thr Ser Gln
 915 920 925
 Leu Ser Ser Gln Val Glu Gln Phe Leu His Arg Asn Ile Gln Glu Tyr
 930 935 940
 Leu Ser Ile Leu Thr Asp Pro Asp Gly Lys Gly Lys Glu Lys Ile Ala
 945 950 955 960
 Glu Leu Ser Ala Thr Ala Gln Glu Ile Ile Lys Ser Gln Ala Ile Ala
 965 970 975
 Thr Lys Lys Ile Ile Ser Asp Tyr His Gln Gln Phe Arg Tyr Lys Leu
 980 985 990
 Gln Asp Phe Ser Asp Gln Leu Ser Asp Tyr Tyr Glu Lys Phe Ile Ala
 995 1000 1005
 Glu Ser Lys Arg Leu Ile Asp Leu Ser Ile Gln Asn Tyr His Thr Phe
 1010 1015 1020
 Leu Ile Tyr Ile Thr Glu Leu Leu Lys Lys Leu Gln Ser Thr Thr Val
 1025 1030 1035 1040
 Met Asn Pro Tyr Met Lys Leu Ala Pro Gly Glu Leu Thr Ile Ile Leu
 1045 1050 1055

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 989 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Asn Ser Lys Gly Thr Arg Ser Ser Val Arg Leu Gln Gly Ala Ser Asn
1 5 10 15

Phe Ala Gly Ile Trp Asn Phe Glu Val Gly Glu Asn Phe Ala Gly Glu
20 25 30

Ala Thr Leu Arg Arg Ile Tyr Gly Thr Trp Glu His Asn Met Ile Asn
35 40 45

His Leu Gln Val Phe Ser Tyr Phe Asp Thr Lys Gly Lys Gln Thr Cys
50 55 60

Arg Ala Thr Leu Glu Leu Ser Pro Trp Thr Met Ser Thr Leu Leu Gln
65 70 75 80

Val His Val Ser Gln Pro Ser Pro Leu Phe Asp Leu His His Phe Asp
85 90 95

Gln Glu Val Ile Leu Lys Ala Ser Thr Lys Asn Gln Lys Val Ser Trp
100 105 110

Lys Ser Glu Val Gln Val Glu Ser Gln Val Leu Gln His Asn Ala His
115 120 125

Phe Ser Asn Asp Gln Glu Val Arg Leu Asp Ile Ala Gly Ser Leu
130 135 140

Glu Gly Gln Leu Trp Asp Leu Glu Asn Phe Phe Leu Pro Ala Phe Gly
145 150 155 160

Lys Ser Leu Arg Glu Leu Leu Gln Ile Asp Gly Lys Arg Gln Tyr Leu
165 170 175

Gln Ala Ser Thr Ser Leu His Tyr Thr Lys Asn Pro Asn Gly Tyr Leu
180 185 190

Leu Ser Leu Pro Val Gln Glu Leu Thr Asp Arg Phe Ile Ile Pro Gly
195 200 205

Leu Lys Leu Asn Asp Phe Ser Gly Ile Lys Ile Tyr Lys Lys Leu Ser
210 215 220

Thr Ser Pro Phe Ala Leu Asn Leu Thr Met Leu Pro Lys Val Lys Phe
225 230 235 240

Pro Gly Val Asp Leu Leu Thr Gln Tyr Ser Lys Pro Glu Gly Ser Ser
245 250 255

Val Pro Thr Phe Glu Thr Thr Ile Pro Glu Ile Gln Leu Thr Val Ser
260 265 270

Gln Phe Thr Leu Pro Lys Ser Phe Pro Val Gly Asn Thr Val Phe Asp
 275 280 285
 Leu Asn Lys Leu Thr Asn Leu Ile Ala Asp Val Asp Leu Pro Ser Ile
 290 295 300
 Thr Leu Pro Glu Gln Thr Ile Glu Ile Pro Ser Leu Glu Phe Ser Val
 305 310 315 320
 Pro Ala Gly Ile Phe Ile Pro Phe Phe Gly Glu Leu Thr Ala His Val
 325 330 335
 Gly Met Ala Ser Pro Leu Tyr Asn Val Thr Trp Ser Thr Gly Trp Lys
 340 345 350
 Asn Lys Ala Asp His Val Glu Thr Phe Leu Asp Ser Thr Cys Ser Ser
 355 360 365
 Thr Leu Gln Phe Leu Glu Tyr Ala Leu Lys Val Val Gly Thr His Arg
 370 375 380
 Ile Glu Asn Asp Lys Phe Ile Tyr Lys Ile Lys Gly Thr Leu Gln His
 385 390 395 400
 Cys Asp Phe Asn Val Lys Tyr Asn Glu Asp Gly Ile Phe Glu Gly Leu
 405 410 415
 Trp Asp Leu Glu Gly Glu Ala His Leu Asp Ile Thr Ser Pro Ala Leu
 420 425 430
 Thr Asp Phe His Leu His Tyr Lys Glu Asp Lys Thr Ser Val Ser Ala
 435 440 445
 Ser Ala Ala Ser Pro Ala Ile Gly Thr Val Ser Leu Asp Ala Ser Thr
 450 455 460
 Asp Asp Gln Ser Val Arg Leu His Val Tyr Phe Arg Pro Gln Ser Pro
 465 470 475 480
 Pro Asp Asn Lys Leu Ser Ile Phe Lys Met Glu Trp Arg Asp Lys Glu
 485 490 495
 Ser Asp Gly Glu Thr Tyr Ile Lys Ile Asn Trp Glu Glu Ala Ala
 500 505 510
 Phe Arg Leu Leu Asp Ser Leu Lys Ser Asn Val Pro Lys Ala Ser Glu
 515 520 525
 Ala Val Tyr Asp Tyr Val Lys Lys Tyr His Leu Gly His Ala Ser Ser
 530 535 540
 Glu Leu Arg Lys Ser Leu Gln Asn Asp Ala Glu His Ala Ile Arg Met
 545 550 555 560

Val Asp Glu Met Asn Val Asn Ala Gln Arg Val Thr Arg Asp Thr Tyr
565 570 575

Gln Ser Leu Tyr Lys Lys Met Leu Ala Gln Glu Ser Gln Ser Ile Pro
580 585 590

Glu Lys Leu Lys Lys Met Val Leu Gly Ser Leu Val Arg Ile Thr Gln
595 600 605

Lys Tyr His Met Ala Val Thr Trp Leu Met Asp Ser Val Ile His Phe
610 615 620

Leu Lys Phe Asn Arg Val Gln Phe Pro Gly Asn Ala Gly Thr Tyr Thr
625 630 635 640

Val Asp Glu Leu Tyr Thr Ile Ala Met Arg Glu Thr Lys Lys Leu Leu
645 650 655

Ser Gln Leu Phe Asn Gly Leu Gly His Leu Phe Ser Tyr Val Gln Asp
660 665 670

Gln Val Glu Lys Ser Arg Val Ile Asn Asp Ile Thr Phe Lys Cys Pro
675 680 685

Phe Ser Pro Thr Pro Cys Lys Leu Lys Asp Val Leu Leu Ile Phe Arg
690 695 700

Glu Asp Leu Asn Ile Leu Ser Asn Leu Gly Gln Gln Asp Ile Asn Phe
705 710 715 720

Thr Thr Ile Leu Ser Asp Phe Gln Ser Phe Leu Glu Arg Leu Leu Asp
725 730 735

Ile Ile Glu Glu Lys Ile Glu Cys Leu Lys Asn Asn Glu Ser Thr Cys
740 745 750

Val Pro Asp His Ile Asn Met Phe Phe Lys Thr His Ile Pro Phe Ala
755 760 765

Phe Lys Ser Leu Arg Glu Asn Ile Tyr Ser Val Phe Ser Glu Phe Asn
770 775 780

Asp Phe Val Gln Ser Ile Leu Gln Glu Gly Ser Tyr Lys Leu Gln Gln
785 790 795 800

Val His Gln Tyr Met Lys Ala Phe Arg Glu Glu Tyr Phe Asp Pro Ser
805 810 815

Val Val Gly Trp Thr Val Lys Tyr Tyr Glu Ile Glu Glu Lys Met Val
820 825 830

Asp Leu Ile Lys Thr Leu Leu Ala Pro Leu Arg Asp Phe Tyr Ser Glu
835 840 845

Tyr Ser Val Thr Ala Ala Asp Phe Ala Ser Lys Met Ser Thr Gln Val
 850 855 860
 Glu Gln Phe Val Ser Arg Asp Ile Arg Glu Tyr Leu Ser Met Leu Ala
 865 870 875 880
 Asp Ile Asn Gly Lys Gly Arg Glu Lys Val Ala Glu Leu Ser Ile Val
 885 890 895
 Val Lys Glu Arg Ile Lys Ser Trp Ser Thr Ala Val Ala Glu Ile Thr
 900 905 910
 Ser Asp Tyr Leu Arg Gln Leu His Ser Lys Leu Gln Asp Phe Ser Asp
 915 920 925
 Gln Leu Ser Gly Tyr Tyr Glu Lys Phe Val Ala Glu Ser Thr Arg Leu
 930 935 940
 Ile Asp Leu Ser Ile Gln Asn Tyr His Met Phe Leu Arg Tyr Ile Ala
 945 950 955 960
 Glu Leu Leu Lys Lys Leu Gln Val Ala Thr Ala Asn Asn Val Ser Pro
 965 970 975
 Tyr Leu Arg Phe Ala Gln Gly Glu Leu Ile Ile Thr Phe
 980 985

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Lys Asp Asn Val Phe Asp Gly Leu Val Arg Val Thr Gln Lys Phe His
 1 5 10 15
 Met Lys Val Lys His Leu Ile Asp Ser Leu Ile Asp Phe Leu Asn Phe
 20 25 30
 Pro Arg Phe Gln Phe Pro Gly Lys Pro Gly Ile Tyr Thr Arg Glu Glu
 35 40 45
 Leu Cys Thr Met Phe Ile Arg Glu Val Gly Thr Val Leu Ser Gln Val
 50 55 60
 Tyr Ser Lys Val His Asn Gly Ser Glu Ile Leu Phe Ser Tyr Phe Gln
 65 70 75 80

Asp	Leu	Val	Ile	Thr	Leu	Pro	Phe	Glu	Leu	Arg	Lys	His	Lys	Leu	Ile
						85					90				95
Asp	Val	Ile	Ser	Met	Tyr	Arg	Glu	Leu	Leu	Lys	Asp	Leu	Ser	Lys	Glu
						100					105				110
Ala	Gln	Glu	Val	Phe	Lys	Ala	Ile	Gln	Ser	Leu	Lys	Thr	Thr	Glu	Val
						115					120				125
Leu	Arg	Asn	Leu	Gln	Asp	Leu	Leu	Gln	Phe	Ile	Phe	Gln	Leu	Ile	Glu
						130					135				140
Asp	Asn	Ile	Lys	Gln	Leu	Lys	Glu	Met	Lys	Phe	Thr	Tyr	Leu	Ile	Asn
						145					150				160
Tyr	Ile	Gln	Asp	Glu	Ile	Asn	Thr	Ile	Phe	Asn	Asp	Tyr	Ile	Pro	Tyr
						165					170				175
Val	Phe	Lys	Leu	Leu	Lys	Glu	Asn	Leu	Cys	Leu	Asn	Leu	His	Lys	Phe
						180					185				190
Asn	Glu	Phe	Ile	Gln	Asn	Glu	Leu	Gln	Glu	Ala	Ser	Gln	Glu	Leu	Gln
						195					200				205
Gln	Ile	His	Gln	Tyr	Ile	Met	Ala	Leu	Arg	Glu	Glu	Tyr	Phe	Asp	Pro
						210					215				220
Ser	Ile	Val	Gly	Trp	Thr	Val	Lys	Tyr	Tyr	Glu	Leu	Glu	Glu	Lys	Ile
						225					230				240
Val	Ser	Leu	Ile	Lys	Asn	Leu	Leu	Val	Ala	Leu	Lys	Asp	Phe	His	Ser
						245					250				255
Glu	Tyr	Ile	Val	Ser	Ala	Ser	Asn	Phe	Thr	Ser	Gln	Leu	Ser	Ser	Gln
						260					265				270
Val	Glu	Gln	Phe	Leu	His	Arg	Asn	Ile	Gln	Glu	Tyr	Leu	Ser	Ile	Leu
						275					280				285
Thr	Asp	Pro	Asp	Gly	Lys	Gly	Lys	Glu	Lys	Ile	Ala	Glu	Leu	Ser	Ala
						290					295				300
Thr	Ala	Gln	Glu	Ile	Ile	Lys	Ser	Gln	Ala	Ile	Ala	Thr	Lys	Lys	Ile
						305					310				320
Ile	Ser	Asp	Tyr	His	Gln	Gln	Phe	Arg	Tyr	Lys	Leu	Gln	Asp	Phe	Ser
						325					330				335
Asp	Gln	Leu	Ser	Asp	Tyr	Tyr	Glu	Lys	Phe	Ile	Ala	Glu	Ser	Lys	Arg
						340					345				350
Leu	Ile	Asp	Leu	Ser	Ile	Gln	Asn	Tyr	His	Thr	Phe	Leu	Ile	Tyr	Ile
						355					360				365

Thr Glu Leu Leu Lys Lys Leu Gln Ser Thr Thr Val Met Asn Pro Tyr
370 375 380
Met Lys Leu Ala Pro Gly Glu Leu Thr Ile Ile Leu
385 390 395

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Ile Pro Gly Leu Ser Glu Lys Tyr Thr Gly Glu Glu Leu Tyr Leu Met
1 5 10 15

Thr Thr Glu Lys Ala Ala Lys Thr Ala Asp Ile Cys Leu Ser Lys Leu
20 25 30

Gln Glu Tyr Phe Asp Ala Leu Ile Ala Ala Ile Ser Glu Leu Glu Val
35 40 45

Arg Val Pro Ala Ser Glu Thr Ile Leu Arg Gly Arg Asn Val Leu Asp
50 55 60

Gln Ile Lys Glu Met Leu Lys His Leu Gln Glu Lys Ile Arg Gln Thr
65 70 75 80

Phe Val Thr Leu Gln Glu Ala Asp Phe Ala Gly Lys Leu Asn Arg Leu
85 90 95

Lys Gln Val Val Gln Lys Thr Phe Gln Lys Ala Gly Asn Met Val Arg
100 105 110

Ser Leu Gln Ser Lys Asn Phe Glu Asp Ile Lys Val Gln Met Gln Gln
115 120 125

Leu Tyr Lys Asp Ala Met Ala Ser Asp Tyr Ala His Lys Leu Arg Ser
130 135 140

Leu Ala Glu Asn Val Lys Lys Tyr Ile Ser Gln Ile Lys Asn Phe Ser
145 150 155 160

Gln Lys Thr Leu Gln Lys Leu Ser Glu Asn Leu Gln Gln Leu Val Leu
165 170 175

Tyr Ile Lys Ala Leu Arg Glu Glu Tyr Phe Asp Pro Thr Thr Leu Gly
180 185 190

Trp Ser Val Lys Tyr Tyr Glu Val Glu Asp Lys Val Leu Gly Leu Leu
 195 200 205
 Lys Asn Leu Met Asp Thr Leu Val Ile Trp Tyr Asn Glu Tyr Ala Lys
 210 215 220
 Asp Leu Ser Asp Leu Val Thr Arg Leu Thr Asp Gln Val Arg Glu Leu
 225 230 235 240
 Val Glu Asn Tyr Arg Gln Glu Tyr Tyr Asp Leu Ile Thr Asp Val Glu
 245 250 255
 Gly Lys Gly Arg Gln Lys Val Met Glu Leu Ser Ser Ala Ala Gln Glu
 260 265 270
 Lys Ile Arg Tyr Trp Ser Ala Val Ala Lys Arg Lys Ile Asn Glu His
 275 280 285
 Asn Arg Gln Val Lys Ala Lys Leu Gln Glu Ile Tyr Gly Gln Leu Ser
 290 295 300
 Asp Ser Gln Glu Lys Leu Ile Asn Val Ala Lys Met Leu Ile Asp Leu
 305 310 315 320
 Thr Val Glu Lys Tyr Ser Thr Phe Met Lys Tyr Ile Phe Glu Leu Leu
 325 330 335
 Arg Trp Phe Glu Gln Ala Thr Ala Asp Ser Ile Lys Pro Tyr Ile Ala
 340 345 350
 Val Arg Glu Gly Glu Leu Arg Ile Asp Val Pro Phe Asp Trp Glu Tyr
 355 360 365
 Ile Asn Gln Met Pro Gln Lys Ser Arg Glu Ala Leu Arg Asn Lys Val
 370 375 380
 Glu Leu Thr Arg Ala Leu Ile Gln Gln Gly Val Glu Gln Gly Thr Arg
 385 390 395 400
 Lys Trp Glu Glu Met Gln Ala Phe Ile Asp Glu Gln Leu Ala Thr Glu
 405 410 415
 Gln Leu Ser Phe Gln Gln Ile Val Glu Asn Ile Gln Lys Arg Met Lys
 420 425 430

Thr

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Asp	Met	Thr	Phe	Ser	Lys	Gln	Asn	Ala	Leu	Leu	Arg	Ser	Glu	Tyr	Gln
1									5			10			15
Ala	Asp	Tyr	Glu	Ser	Leu	Arg	Phe	Phe	Ser	Leu	Leu	Ser	Gly	Ser	Leu
									20			25			30
Asn	Ser	His	Gly	Leu	Glu	Leu	Asn	Ala	Asp	Ile	Leu	Gly	Thr	Asp	Lys
									35			40			45
Ile	Asn	Ser	Gly	Ala	His	Lys	Ala	Thr	Leu	Arg	Ile	Gly	Gln	Asp	Gly
									50			55			60
Ile	Ser	Thr	Ser	Ala	Thr	Thr	Asn	Leu	Lys	Cys	Ser	Leu	Leu	Val	Leu
								65			70			75	80
Glu	Asn	Glu	Leu	Asn	Ala	Glu	Leu	Gly	Leu	Ser	Gly	Ala	Ser	Met	Lys
								85			90			95	
Leu	Thr	Thr	Asn	Gly	Arg	Phe	Arg	Glu	His	Asn	Ala	Lys	Phe	Ser	Leu
								100			105			110	
Asp	Gly	Lys	Ala	Ala	Leu	Thr	Glu	Leu	Ser	Leu	Gly	Ser	Ala	Tyr	Gln
								115			120			125	
Ala	Met	Ile	Leu	Gly	Val	Asp	Ser	Lys	Asn	Ile	Phe	Asn	Phe	Lys	Val
								130			135			140	
Ser	Gln	Glu	Gly	Leu	Lys	Leu	Ser	Asn	Asp	Met	Met	Gly	Ser	Tyr	Ala
								145			150			155	160
Glu	Met	Lys	Phe	Asp	His	Thr	Asn	Ser	Leu	Asn	Ile	Ala	Gly	Leu	Ser
								165			170			175	
Leu	Asp	Phe	Ser												
								180							

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Asp	Leu	Thr	Phe	Ser	Lys	Gln	Asn	Ala	Leu	Leu	Arg	Ala	Glu	Tyr	Gln
1									5			10			15

Ala	Asp	Tyr	Lys	Ser	Leu	Arg	Phe	Phe	Thr	Leu	Leu	Ser	Gly	Leu	Leu
20							25					30			
Asn	Thr	His	Gly	Leu	Glu	Leu	Asn	Ala	Asp	Ile	Leu	Gly	Thr	Asp	Lys
35					40							45			
Met	Asn	Thr	Ala	Ala	His	Lys	Ala	Thr	Leu	Arg	Ile	Gly	Gln	Asn	Gly
50					55						60				
Val	Ser	Thr	Ser	Ala	Thr	Thr	Ser	Leu	Arg	Tyr	Ser	Pro	Leu	Met	Leu
65					70					75			80		
Glu	Asn	Glu	Leu	Asn	Ala	Glu	Leu	Ala	Leu	Ser	Gly	Ala	Ser	Met	Lys
					85					90			95		
Leu	Ala	Thr	Asn	Gly	Arg	Phe	Lys	Glu	His	Asn	Ala	Lys	Phe	Ser	Leu
					100				105			110			
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Glu	Leu	Ser	Leu	Gly	Ser	Ala	Tyr	Gln
					115				120			125			
Ala	Met	Ile	Leu	Gly	Ala	Asp	Ser	Lys	Asn	Ile	Phe	Asn	Phe		
					130				135			140			

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

His	Ile	Phe	Ile	Pro	Ala	Met	Gly	Asn	Ile	Thr	Tyr	Asp	Phe	Ser	Phe
1						5				10				15	
Lys	Ser	Ser	Val	Ile	Thr	Leu	Asn	Thr	Asn	Ala	Glu	Leu	Phe	Asn	Gln
					20					25			30		
Ser	Asp	Ile	Val	Ala	His	Leu	Leu	Ser	Ser	Ser	Ser	Val	Ile	Asp	
					35			40				45			
Ala	Leu	Gln	Tyr	Lys	Leu	Glu	Gly	Thr	Thr	Arg	Leu	Thr	Arg	Lys	Arg
					50			55			60				
Gly	Leu	Lys	Leu	Ala	Thr	Ala	Leu	Ser	Leu	Ser	Asn	Lys	Phe	Val	Glu
					65			70			75		80		
Gly	Ser	His	Asn	Ser	Thr	Val	Ser	Leu	Thr	Thr	Lys	Asn	Met	Glu	Val
					85			90			95				

Ser Val Ala Lys Thr Thr Lys Ala Glu Ile Pro Ile Leu Arg Met Asn
100 105 110

Phe Lys Gln Glu Leu Asn Gly Asn Thr Lys Ser Lys Pro Thr Val Ser
115 120 125

Ser Ser Met Glu Phe Lys Tyr Asp Phe Asn Ser Ser Met Leu Tyr Ser
130 135 140

Thr Ala Lys Gly Ala Val Asp His Lys Leu Ser Leu Glu Ser Leu Thr
145 150 155 160

Ser Tyr Phe Ser Ile Glu Ser Ser Thr Lys Gly Asp Val Lys Gly Ser
165 170 175

Val Leu Ser Arg Glu Tyr Ser Gly Thr Ile Ala Ser Glu Ala Asn Thr
180 185 190

Tyr Leu Asn Ser Lys Ser Thr Arg Ser Ser Val Lys Leu Gln Gly Thr
195 200 205

Ser Lys Ile Asp Asp Ile Trp Asn Leu Glu Val Lys Glu Asn Phe Ala
210 215 220

Gly Glu Ala Thr Leu Gln Arg Ile Tyr Ser Leu Trp Glu His Ser Thr
225 230 235 240

Lys Asn His Leu Gln Leu Glu Gly Leu Phe Phe Thr Asn Gly Glu His
245 250 255

Thr Ser Lys Ala Thr Leu Glu Leu Ser Pro Trp Gln Met Ser Ala Leu
260 265 270

Val Gln Val His Ala Ser Gln Pro Ser Ser Phe His Asp Phe Pro Asp
275 280 285

Leu Gly Gln Glu Val Ala Leu Asn Ala Asn Thr Lys Asn Gln Lys Ile
290 295 300

Arg Trp Lys Asn Glu Val Arg Ile His Ser Gly Ser Phe Gln Ser Gln
305 310 315 320

Val Glu Leu Ser Asn Asp Gln Glu Lys Ala His Leu Asp Ile Ala Gly
325 330 335

Ser Leu Glu Gly His Leu Arg Phe Leu Lys Asn Ile Ile Leu Pro Val
340 345 350

Tyr Asp Lys Ser Leu Trp Asp Phe Leu Lys Leu Asp Val Thr Thr Ser
355 360 365

Ile Gly Arg Arg Gln His Leu Arg Val Ser Thr Ala Phe Val Tyr Thr
370 375 380

Lys Asn Pro Asn Gly Tyr Ser Phe Ser Ile Pro Val Lys Val Leu Ala
385 390 395 400

Asp Lys Phe Ile Thr Pro Gly Leu Lys Leu Asn Asp Leu Asn Ser Val
405 410 415

Leu Val Met Pro
420

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met Ala Ser Glu Lys Gly Pro Ser Asn Lys Asp Tyr Thr Leu Arg Arg
1 5 10 15

Arg Ile Glu Pro Trp Glu Phe Glu Val Phe Phe Asp Pro Gln Glu Leu
20 25 30

Arg Lys Glu Ala Cys Leu Leu Tyr Glu Ile Lys Trp Gly Ala Ser Ser
35 40 45

Lys Thr Trp Arg Ser Ser Gly Lys Asn Thr Thr Asn His Val Glu Val
50 55 60

Asn Phe Leu Glu Lys Leu Thr Arg Lys Glu Ala Cys Leu Leu Tyr Glu
65 70 75 80

Ile Lys Trp Gly Ala Ser Ser Lys Thr Trp Arg Ser Ser Gly Lys Asn
85 90 95

Thr Thr Asn His Val Glu Val Asn Phe Leu Glu Lys Leu Thr Ser Glu
100 105 110

Gly Arg Leu Gly Pro Ser Thr Cys Cys Ser Ile Thr Trp Phe Leu Ser
115 120 125

Trp Ser Pro Cys Trp Glu Cys Ser Met Ala Ile Arg Glu Phe Leu Ser
130 135 140

Gln His Pro Gly Val Thr Leu Ile Ile Phe Val Ala Arg Leu Phe Gln
145 150 155 160

His Met Asp Arg Arg Asn Arg Gln Gly Leu Lys Asp Leu Val Thr Ser
165 170 175

Gly Val Thr Val Arg Val Met Ser Val Ser Glu Tyr Cys Tyr Cys Trp
 180 185 190
 Glu Asn Phe Val Asn Tyr Pro Pro Gly Lys Ala Ala Gln Trp Pro Arg
 195 200 205
 Tyr Pro Pro Arg Trp Met Leu Met Tyr Ala Leu Glu Leu Tyr Cys Ile
 210 215 220
 Ile Leu Gly Leu Pro Pro Cys Leu Lys Ile Ser Arg Arg His Gln Lys
 225 230 235 240
 Gln Leu Thr Phe Phe Ser Leu Thr Pro Gln Tyr Cys His Tyr Lys Met
 245 250 255
 Ile Pro Pro Tyr Ile Leu Leu Ala Thr Gly Leu Leu Gln Pro Ser Val
 260 265 270
 Pro Trp Arg
 275

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGATCTGACG GTTCACTAAA CCAGCTCTGC TTATATAGAC CTCCCACCGT ACACGCCTAC	60
CGCCCATTG CGTCAATGGG GCGGAGTTGT TACGACATTT TGGAAAGTCC CGTTGATTTT	120
GGTGCCAAAA CAAACTCCAT TGACGTCAAT GGGGTGGAGA CTTGGAAATC CCCGTGAGTC	180
AAACCGCTAT CCACGCCAT TGATGTACTG CCAAAACCGC ATCACCATGG TAATAGCGAT	240
GACTAATACG TAGATGTACT GCCAAGTAGG AAAGTCCAT AAGGTCATGT ACTGGCATA	300
ATGCCAGGCG GGCCATTAC CGTCATTGAC GTCAATAGGG GGCGTACTTG GCATATGATA	360
CACTTGATGT ACTGCCAAGT GGGCAGTTA CCGTAAATAC TCCACCCATT GACGTCAATG	420
GAAAGTCCCT ATTGGCGTTA CTATGGGAAC ATACGTCATT ATTGACGTCA ATGGGCGGGG	480
GTCGTTGGGC GGTCAGCCAG GCGGGCCATT TACCGTAAGT TATGTAACGC GGAACCTCCAT	540
ATATGGGCTA TGAACTAATG ACCCCGTAAT TGATTACTAT TAATAACTA	589

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GATCCAAATC ACCCACTGCA ACTCCTCCCC CTGCG

35

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GATCCATCCA ATTGGGCAAT CAGGAG

26

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GATCCGGTCT CCAATTGG

18

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GATCCTCGGG AAAGGGAAAC CGAAACTGAA GCCG

34